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DN nucleic - nucleic search, using sw model

run on: January 31, 2004, 00:52:19 ; Search time 114 Seconds

(without alignments)
7035.028 Million cell updates/sec

Title: US-09-890-456-8

Perfect score: 1817
Sequence: 1 99acacataaaaggaaaca.....aagttcataaccatcaaaa 1817

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	196.4	10.8	2315	4	US-09-152-060-48
C 2	194.2	10.7	3856	4	US-09-620-312D-451
C 3	88.8	4.9	1732	4	US-09-152-060-30
C 4	49.6	2.7	4453	4	US-09-146-053-5
C 5	48	2.6	66804	4	US-09-740-041-3
C 6	47.6	2.6	703	3	US-09-313-300-6
C 7	44.8	2.5	5824	4	US-09-620-312D-72
C 8	44.4	2.4	50000	4	US-09-146-053-3
C 9	42.4	2.3	81001	4	US-09-750-580-1
C 10	42	2.3	2897	4	US-09-620-312D-401
C 11	41.6	2.3	62804	4	US-09-800-960-3
C 12	41	2.3	10627	1	US-08-060-925A-12
C 13	41	2.3	51719	4	US-09-318-686-2
C 14	41	2.3	92139	4	US-09-318-686-1
C 15	40.8	2.2	18853	4	US-09-820-005-3
C 16	40.8	2.2	51719	4	US-09-318-686-2
C 17	40.8	2.2	92139	4	US-09-318-686-1
C 18	40.6	2.2	6953	1	US-07-805-123C-2
C 19	40.6	2.2	6953	1	US-08-033-081B-2
C 20	40.6	2.2	7301	4	US-09-816-094-3
C 21	40.6	2.2	36741	3	US-09-301-665-3
C 22	40.6	2.2	50000	4	US-09-146-053-3
C 23	40.6	2.2	55298	4	US-08-191-355C-1
C 24	40.4	2.2	1601	4	US-09-420-133A-182
C 25	39.6	2.2	44553	4	US-09-146-053-5
C 26	39.2	2.2	377	3	US-09-328-111-672
C 27	39.2	2.2	1454	1	US-08-467-155A-2

C 28	39.2	2.2	1454	2	US-08-628-198-2	Sequence 2, Appli
C 29	39.2	2.2	1454	3	US-09-201-038-2	Sequence 2, Appli
C 30	39.2	2.2	1454	5	PCT-US96-07343-2	Sequence 2, Appli
C 31	39.2	2.2	7218	1	US-08-232-463-14	Sequence 14, Appli
C 32	39.2	2.2	24707	4	US-09-740-027-3	Sequence 3, Appli
C 33	39	2.1	3796	1	US-08-343-760A-1	Sequence 1, Appli
C 34	39	2.1	10014	3	US-08-927-219-130	Sequence 130, App
C 35	38.8	2.1	441	4	US-09-288-143-59	Sequence 59, Appli
C 36	38.8	2.1	11725	2	US-08-756-506-1	Sequence 12, Appli
C 37	38.6	2.1	4129	3	US-08-370-319C-12	Sequence 12, Appli
C 38	38.6	2.1	4129	3	US-09-224-834-12	Sequence 4, Appli
C 39	38.6	2.1	50000	4	US-09-146-053-4	Sequence 3, Appli
C 40	38.6	2.1	111282	4	US-08-754-250-3	Sequence 3, Appli
C 41	38.4	2.1	15063	4	US-08-801-032-3	Sequence 3, Appli
C 42	38.2	2.1	17138	3	US-09-813-819-3	Sequence 3, Appli
C 43	38.2	2.1	17138	4	US-09-820-048-3	Sequence 3, Appli
C 44	38.2	2.1	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 45	38.2	2.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-152-060-48/c
; Sequence 48 Application US/09152060
; Patent No 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2264)
; OTHER INFORMATION: n equals a.t.g. or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2312)
; OTHER INFORMATION: n equals a.t.g. or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2315)
; OTHER INFORMATION: n equals a.t.g. or c
US-09-152-060-48

Query Match 10.8%; Score 196.4; DB 4; Length 2315;
Best Local Similarity 53.0%; Pred. No. 4.8e-48;
Matches 475; Conservative 0; Mismatches 406; Indels 15; Gaps 2;

2Y 475 CAGACATGTTCTGCTTTTCATCGGAAGAGATACTCCCGCGGAGAGAGCTGGCACCCCT 534
Db 2063 CAGAGACATATGCTATGTTTCAAGACAAAGATACAGAGTGGGTGAGAGATGGCATCCTT 2004

2Y 535 ACTTGGAGCCACAGAGCTGATGACTGCTGGCTGTACCTGTCTCAGAGGGCGGCCCATG 594
Db 2003 ACCTGGAACTTATGGGTGTTTACTTGGCTGAACTGCTATCTCTCAGAGATGGGAATG 1944

2Y 595 TGAGTTGTACCGCTTCACTGTCCGCTGTCACTGTGCCCCAGCTGTGACGGAGCCAC 654
Db 1943 TGCCTTTCAGCCGAGTACAGATGTCCTCAAAATGTTTCAATGCTCTTCTCTGTCATATTCCTC 1884

2Y 655 AGCAATCTGTCCCAAGTGTGTGGAACCTCACACTCTCTCTGGAAGTCTCTGAGTCTG 711
Db 1883 ATCTGTCTGCTCCCTGCTGCCAGAGACTCTCTTACCCCGAGTGAACTAATAGGTGACCA 1824

2Y 712 CAATAGTCTGCCAGACAAAGGAGACCATGTACCAACAGAGAGATCTTCAGTGGCCCATG 771
Db 1823 GCAAGTCTTGGAGTACAAATGGGACAACTTACCAACATGAGAGAGCTGTCTGTAAGTGAAG 1764

2Y 772 AGCTGTTCCCTCCGCTGCCCAACAGTGTGTCTCTGAGCTGTGCAGAGTGCACAGAGGGCCAGA 831
Db 1763 GCCTCTTTCAGAAATCGGACCCCAATCAATGACCCAGTGCAGCTGTTCGGAGGGAAAG 1704

2Y 832 TCTACTGGCGCTCAACACTGCTGCCCGGACCCAGGCTGCCAGACCCCTCTCGCTGCCAG 891
Db 1703 TGTATTGTGCTCAAGACTTGCCTCCCAAAATTAACCTGTGCTCTCCCAAGTCTGTGTCAG 1644

2Y 892 ACTCTCTGCTCCCAAGCTTCAAAAGATGAGGCAAGTACGCAATCGGATGAAGAGGACATG 951
Db 1643 ATTCTCTGCTCCGGGTATGACAGAGAGATGGAGAACTGTTCATGGGAACTTCTGATGGT 1584

2Y 952 TGCAGTGCCTCCA-----TGGGTGAGACATCCTCAGGATCCATGTTCAGTGT 999
Db 1583 ATATCTTCGGCAACCTGCCAACACAGAGACGAACATTTTACACGGCTCTCACTATG 1524

2Y 1000 ATGCTGGAGAAAGAGAGCGCGCGGACCCAGCCAGCTGCCAGACCCCTCTCGCTCTGA 1059
Db 1523 ATCTCTCAACAGCCAGAGCTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464

2Y 1060 GCTTCACTCTTCGCTTCACTTCAAGCCAGGAGGACAGGAGCAACTGTTCAGATGCTGCC 1119
Db 1463 GGGGAGCTCTTATGGATTCCTCAGCAAGCATCAGGAACTTGTGCAAAATGTTCATCAATA 1404

2Y 1120 TGAAGGAGAAACATAAGAAAGCTGTGTGATGCGCGGGAAGACGCTACTCCACGGGAGG 1179
Db 1403 ACAAAACAAGACATGGAACAAAGTGTGTGTTTCCAATGGAAGACCTTATCTCATGGCAGT 1344

2Y 1180 TGTGACACCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1239
Db 1343 CTGTGACACCAACCTCCGGAATTTGGCAATTTGGAGTGTGTGTAATGTAATGTAATG 1284

2Y 1240 ATGGCGCGGAGGACTGCGAGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299
Db 1283 TCACCAAGCAAGATGTAAAGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224

2Y 1300 AGAAATGGCTGGGAAGTGTGCAAGATTTGCCAGAGACAAAGCAGACCTGGC 1355
Db 1223 AAAAAATAGCGGAAATGTGCAAGGTGTGTCCAGAGAACTTCCAGAGCAAGC 1168

RESULT 2

US-09-620-312D-451
; Sequence 451, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chonghua
; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungling
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP23
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 451
; LENGTH: 3856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (105)..(1481)
US-09-620-312D-451

Query Match 10.7%; Score 194.2; DB 4; Length 3856;
Best Local Similarity 53.0%; Pred. No. 2.9e-47;
Matches 471; Conservative 0; Mismatches 403; Indels 15; Gaps 2;

QY 475 CAGACATGTTCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGTGGCACCCCT 534
Db 202 CAGAGACATATTCATGTTTCAAGACAAAGATGACAGAGTGGGTGAGAGATGCTCTT 261

QY 535 ACTTGGAGCCACAGAGCTGTACTGCTGCTGCTGTACTGTCTGCTGCTGCTGCTGCTGCTG 594
Db 262 ACTTGGAGCCATATGAGTGTGTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321

QY 595 TGAGTTGTACCGCTTCACTGTGCGCTGTCCACTGCCCCCGAGCTGTGACGGAGCCAC 654
Db 322 TGTCTTGGAGCGGAGTACAGTGTCAAAATGTTTCAATGCTTCTCTCTCTGCTGCTGCTGCT 381

QY 655 AGCAATGCTGTCCCAAGTGTGTGGAACCTCACTCTCTCTCTGGAATC---CGGCGCCAC 711
Db 382 ATCTGTGCTGCTCCCTGCTGCCAGAGACTCTTACCCCGAGTGAACAAATAAGTGAACA 441

QY 712 CAAAGTCTCTGCGAGACAAAGGAGCCATGTACCAACAGAGAGATCTTTCAGTGGCCATG 771
Db 442 GCAAGTCTTGGAGTACAAATGGAGCAACTTACCAACATGAGAGAGTGTTCGTAGCTGAAG 501

QY 772 AGCTGTTCCCTCCGCTGCCCAACAGTGTGTCTCTGCTGAGCTGACACAGAGGGCCAGA 831
Db 502 GCTCTTTTCAGATCGGCAACCCCAATCAATGACCCAGTGCAGCTGTTCGGAGGGAAAG 561

QY 832 TCTACTGGCGCTCAACACTGCTGCCCGGACCCAGGCTGCCAGCACTCTCTCTCTCTCTCT 891
Db 562 TGTATTGTGCTCAAGACTTGTCCCAAAATTAACCTGTGCTCTCTCTCTCTCTCTCTCT 621

QY 892 ACTCTGCTGCCAAGCTGCTCAAGATGAGGCAAGTGAACATCGGATGAGAGAGACATG 951
Db 622 ATTCTGCTGCGGGTATGACAGAGAGATGGAGAACTGTCAATGGGAACTTCTGATGGTG 681

QY 952 TGCAGTCTGCTCCA-----TGGGGTGAAGATCTCTCAGGATCCATGTTCCAGTG 999
Db 682 ATATCTTCCGGAACCTTGCCAAAGAGCAAGCAATTTTACCAACGCTCTCTCACTATG 741

Sequence 3, Application US/09740041
Patent No. 6562593
GENERAL INFORMATION:
APPLICANT: MERKULOV, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001001
CURRENT APPLICATION NUMBER: US/09/740,041
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 66804
TYPE: DNA
ORGANISM: Human
S-09-740-041-3
Query Match 2.6%; Score 48; DB 4; Length 66804;
Best Local Similarity 84.4%; Pred. No. 0.0036;
Matches 54; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
b 5244 TTACATGAGAACTGAGGCACAGAGAGGTAAAGTCTTCCCAAGGTCACACAGCT 5303
Y 1564 AGAA 1567
b 5304 ATAA 5307
RESULT 6
US-09-313-300-6
Sequence 6, Application US/09313300
Patent No. 622027
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew, R.
APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
APPLICANT: Tang, Tom, Y.
APPLICANT: Baughn, Mariah, R.
APPLICANT: Azimzal, Valda
TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
FILE REFERENCE: PB-0012 US
CURRENT APPLICATION NUMBER: US/09/313,300
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 703
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 1941247
OTHER INFORMATION: 1941247
PUBLICATION INFORMATION:
US-09-313-300-6
Query Match 2.6%; Score 47.6; DB 3; Length 703;
Best Local Similarity 85.5%; Pred. No. 0.00037;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
b 554 TTACATGAGAACTGAGGCACAGAGAGGTAAAGTCTTCCCAAGGTCACACAGCG 613
Y 1564 AG 1565
b 614 AG 615
RESULT 7
US-09-620-312D-72/c

Sequence 72, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 72
LENGTH: 5824
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (590)..(5824)
US-09-620-312D-72
Query Match 2.5%; Score 44.8; DB 4; Length 5824;
Best Local Similarity 81.2%; Pred. No. 0.0082;
Matches 52; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Y 1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
b 139 TGATAGATGAGAACTGAGAACTCAGAGAGGTAAAGTATCTTGGCCCAAGGTCACACAGCT 80
Y 1564 AGAA 1567
b 79 AGTA 76
RESULT 8
US-09-146-053-3
Sequence 3, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,854
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens

US-09-146-053-3

Query Match 2.4%; Score 44.4; DB 4; Length 50000;
Best Local Similarity 82.3%; Pred. No. 0.0367;
Matches 51; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1504 TAAAGATGAGGAACTGAGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCACACAGCC 1563
Db 18961 TTACAGATGAGGACATTGAGGCTCAGAGAGGTCAACACAGGTTCCTCAAGCCACACAGCC 19020

Qy 1564 AG 1565
Db 19021 AG 19022

RESULT 9

US-09-750-580-1/C
Sequence 1, Application US/09750580
Patent No. 6455280
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bilhain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2.CIP
CURRENT APPLICATION NUMBER: US/09750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 10945..12946
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc feature
LOCATION: 15969..17969
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T

NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
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LOCATION: 76844..76864
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind

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; OTHER INFORMATION: 20-841-149.mis complement
; NAME/KEY: primer.bnd
; LOCATION: 45423..45441
; OTHER INFORMATION: 20-842-115.mis
; NAME/KEY: primer.bnd
; LOCATION: 45443..45461
; OTHER INFORMATION: 20-842-115.mis complement
; NAME/KEY: primer.bnd
; LOCATION: 77039..77057
; OTHER INFORMATION: 20-853-415.mis
; NAME/KEY: primer.bnd
; LOCATION: 77059..77077
; OTHER INFORMATION: 20-853-415.mis complement
; NAME/KEY: misc.binding
; LOCATION: 1227..1251
; OTHER INFORMATION: 20-828-311.probe
; NAME/KEY: misc.binding
; LOCATION: 12335..12359
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc.binding
; LOCATION: 15229..15253
; OTHER INFORMATION: 17-41-250.probe
; NAME/KEY: misc.binding
; LOCATION: 42205..42230
; OTHER INFORMATION: 20-841-149.probe
; NAME/KEY: misc.binding
; LOCATION: 45430..45454
; OTHER INFORMATION: 20-842-115.probe
; NAME/KEY: misc.binding
; LOCATION: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
; OTHER INFORMATION: 20-853-415.probe
; US-09-750-580-1

Query Match          2.3%; Score 42.4; DB 4; Length 81001;
Best Local Similarity 81.7%; Pred. No. 0.19;
Matches 49; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1504 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 33792 TTATAGATAAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 33733

RESULT 10
US-09-620-312D-401
; Sequence 401, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2a
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PC_FL_Genes Version 1.0
; SEQ ID NO 401
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(1136)
; US-09-620-312D-401

Query Match          2.3%; Score 42; DB 4; Length 2697;
Best Local Similarity 77.3%; Pred. No. 0.036;
Matches 51; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1508 AGATGAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
DB 104 AGATGAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGTG 163

QY 1568 TCTTCC 1573
DB 164 TGAACC 169

RESULT 11
US-09-800-960-3
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)....(62804)
; OTHER INFORMATION: n = A,T,C or G
; US-09-800-960-3

Query Match          2.3%; Score 41.6; DB 4; Length 62804;
Best Local Similarity 78.1%; Pred. No. 0.28;
Matches 50; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1504 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 36676 TTATAGATAAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCT 36735

QY 1564 AGAA 1567
DB 36736 GGCA 36739

RESULT 12
US-08-060-925A-12
; Sequence 12, Application US/08060925A
; Patent No. 5439824
; GENERAL INFORMATION:
; APPLICANT: Brantley, Mark
; APPLICANT: Laubach, Victor
; TITLE OF INVENTION: INCREASED EXPRESSION OF ALPHA-1
; TITLE OF INVENTION: ANTI-TRYPsin IN EXPRESSION VECTORS THROUGH THE INCLUSION OF
; TITLE OF INVENTION: INTRON II
; NUMBER OF SEQUENCES: 12
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: KNOBE, MARTENS, OLSON AND BEAR
;; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
;; CITY: NEWPORT BEACH
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/060,925A
;; FILING DATE: 06-MAY-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fuller, Michael L.
;; REGISTRATION NUMBER: 36,516
;; REFERENCE/DOCKET NUMBER: NH040.001A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-235-8550
;; TELEFAX: 619-235-0176
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10627 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEITICAL: NO
;; ANTI-SENSE: NO
;; US-08-060-925A-12

Query Match 2.3%; Score 41; DB 1; Length 10627;
Best Local Similarity 82.5%; Pred. No. 0.16;
Matches 47; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

2y 1513 AGGAACCTGAGGTCAGAGAGGTCAGAGTACCTGGCCCAAGGCCACACAGCCAGAAATC 1569
Db 1687 AGGAACCTGAGGTCAGAGAGGTTAAGTAACTGTGTCACAGCTTACACAGCTAATAGC 1743

RESULT 13
US-09-918-686-2/C
; Sequence 2, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proell, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 51719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1246..2572, 2604
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-2

Query Match 2.3%; Score 41; DB 4; Length 51719;
Best Local Similarity 76.9%; Pred. No. 0.38;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: KNOBE, MARTENS, OLSON AND BEAR
;; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
;; CITY: NEWPORT BEACH
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/060,925A
;; FILING DATE: 06-MAY-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fuller, Michael L.
;; REGISTRATION NUMBER: 36,516
;; REFERENCE/DOCKET NUMBER: NH040.001A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-235-8550
;; TELEFAX: 619-235-0176
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10627 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHEITICAL: NO
;; ANTI-SENSE: NO
;; US-08-060-925A-12

Query Match 2.3%; Score 41; DB 4; Length 92139;
Best Local Similarity 76.9%; Pred. No. 0.52;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1507 AAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGA 1566
Db 41491 AAGATGAGGAAACTAAGGATTAAGGAGGGGTTAAGTAACTTTTTCAGGTACACAGCTAGC 41432

Qy 1567 ATCTT 1571
Db 41431 AAATT 41427

RESULT 14
US-09-918-686-1/C
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proell, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7045..8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 2.3%; Score 41; DB 4; Length 92139;
Best Local Similarity 76.9%; Pred. No. 0.52;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1507 AAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGA 1566
Db 47288 AAGATGAGGAAACTAAGGATTAAGGAGGGGTTAAGTAACTTTTTCAGGTACACAGCTAGC 47229

Qy 1567 ATCTT 1571
Db 47228 AAATT 47224

RESULT 15
US-09-820-005-3
; Sequence 3, Application US/09820005
; Patent No. 6489149
; GENERAL INFORMATION:
; APPLICANT: SHAO, Wei et al
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; FILE REFERENCE: CL001198
; CURRENT APPLICATION NUMBER: US/09/820,005
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18853
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(18853)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-005-3

Query Match 2.2%; Score 40.8; DB 4; Length 18853;

Best Local Similarity 80.0%; Pred. No. 0.25; DB 4; Length 51719;
Matches 48; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1508 AGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGGGCCCAAGGCCACAGCCAGAA 1567
7538 AGATGAGAAACCAAGGCTCAGAGAGGAAAGCCACTTCCAGAGCCACAGCCAGAA 7597

RESULT 16
US-09-918-686-2
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Prohl, Sean
; APPLICANT: Paepel, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 51719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1246, 2572, 2604
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-2

Query Match 2.2%; Score 40.8; DB 4; Length 51719;
Best Local Similarity 67.9%; Pred. No. 0.43; DB 4; Length 51719;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
1491 CTCCTGGAAGCTGTTAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCA 1550
24678 CTGGCAAGGCTTACAGGTGGGAATCGAGGCACAGAGAGGTAAAGTAGCTTGCCTA 24737
1551 AGGCCACACAGCCAGATCTTCCA 1574
24738 AGATCACCAGTAGTAAGTAGCA 24761

RESULT 17
US-09-918-686-1
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Prohl, Sean
; APPLICANT: Paepel, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 2.2%; Score 40.8; DB 4; Length 92139;
Best Local Similarity 67.9%; Pred. No. 0.6; DB 4; Length 92139;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
1491 CTCCTGGAAGCTGTTAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCA 1550
30475 CTGGCAAGGCTTACAGGTGGGAATCGAGGCACAGAGAGGTAAAGTAGCTTGCCTA 30534
1551 AGGCCACACAGCCAGATCTTCCA 1574
30535 AGATCACCAGTAGTAAGTAGCA 30558

RESULT 18
US-07-805-123C-2/c
; Sequence 2, Application US/07805123C
; Patent No. 5262529
; GENERAL INFORMATION:
; APPLICANT: Dryla, Thaddeus P.
; APPLICANT: Berson, Eliot L.
; TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL
; TITLE OF INVENTION: DEGENERATIVE DISEASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/805,123C
; FILING DATE: 19911211
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/469,215
; FILING DATE: January 24, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/069003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6953
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-805-123C-2

Query Match 2.2%; Score 40.6; DB 1; Length 6953;
Best Local Similarity 64.3%; Pred. No. 0.16; DB 1; Length 6953;
Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
1480 TGGAGATCTACTCTCGAAGCTGGTAAAGATGAGAACTGAGGCTCAGAGAGGTGAAG 1539
4882 TGGTGTGTCCTTCTACCTTCTATGGATGAGGAACCAAGCAAGAGAGGAAT 4823
1540 TACCTGGCCCAAGGCCACAGCCAGATCTTCCA 1574
4822 TGACTTGGCCAGGGCCATACAGCTAGAAATGGCA 4788

RESULT 19
US-08-033-081B-2/c


```

: Sequence 2, Application US/08033081B
: Patent No. 5495421
: GENERAL INFORMATION:
: APPLICANT: Dryja, Thaddeus P.
: APPLICANT: Berzon, Elliot L.
: TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL
: TITLE OF INVENTION: DEGENERATIVE DISEASES
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: COMPUTER: IBM PS/2 Model 50Z or 55SX
: OPERATING SYSTEM: MS-DOS (Version 5.0)
: SOFTWARE: WordPerfect (Version 5.1)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/033,081B
: FILING DATE: March 11, 1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/825,296
: FILING DATE: January 23, 1992
: APPLICATION NUMBER: 07/469,215
: FILING DATE: January 24, 1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 00246/069005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: (617) 542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6953
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
: IS-08-033-081B-2
:
: Query Match 2.2%; Score 40.6; DB 1; Length 6953;
: Best Local Similarity 64.2%; Pred. No. 0.16;
: Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
:
: Y 1480 TGGAGATCTACTCTGGGAAGCTGCTAAAGATGAGGAAATCAGCGCTCAGAGGTTGAAG 1539
: b 4882 TGGTGTTCCTTCCTTACCTTCTATGATGAGGAACCAACAGCAGAGGAAT 4823
:
: Y 1540 TACTGGCCCAAGGCCACAGCAGCAATCTTCCA 1574
: b 4822 TGACTTCCCAAGGCCATACAGCTAGAAATGGCA 4798
:
: RESULT 20
: IS-09-816-094-3/c
: Sequence 3, Application US/09816094
: Patent No. 6534299
: GENERAL INFORMATION:
: APPLICANT: Wei, Ming-Hui et al.
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CL000536-CIP
: CURRENT APPLICATION NUMBER: US/09/816,094
: CURRENT FILING DATE: 2001-03-26
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3

```

Query Match 2.2%; Score 40.6; DB 4; Length 50000;
Best Local Similarity 73.2%; Pred. No. 0.49;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 14909 TTAATCTGAGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCT 14850

QY 1564 AGAATCTTCCA 1574
DB 14849 AGGATGTGCCA 14839

RESULT 23
US-09-491-356C-1/c
; Sequence 1, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Gibbs, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083.465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 55298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (838)..(838)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (16728)..(16728)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (22750)..(22750)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (22756)..(22756)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (28519)..(28519)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (44804)..(44804)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (45002)..(45002)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (54049)..(54049)
; OTHER INFORMATION: n is not determined
; NAME/KEY: misc.feature
; LOCATION: (54226)..(54226)
; OTHER INFORMATION: n is not determined
US-09-491-356C-1

Query Match 2.2%; Score 40.6; DB 4; Length 55298;
Best Local Similarity 73.2%; Pred. No. 0.51;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 35231 TCATCTGATGGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCT 35172

QY 1564 AGAATCTTCCA 1574
DB 35171 AGGAAGTGCTA 35161

RESULT 24
US-09-220-132-182
; Sequence 182, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shvjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220.132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-220-132-182

Query Match 2.2%; Score 40.4; DB 4; Length 1601;
Best Local Similarity 75.8%; Pred. No. 0.081;
Matches 50; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCC 1563
DB 181 TACAGACAGGAGAGCTGAAGCACAGAGAGGTTAAGTGACTTGCCCAAGGTCACACAGTT 240

QY 1564 AGAATC 1569
DB 241 AATTC 246

RESULT 25
US-09-146-053-5/c
; Sequence 5, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146.053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 44453
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-146-053-5

Query Match 2.2%; Score 39.6; DB 4; Length 44453;
Best Local Similarity 77.4%; Pred. No. 0.9;
Matches 48; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAAGTACCTGGCCCAAGGCCACACAGCC 1563

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> 31158 TTACAGAGAACTGAAGCAGACAGAGGCTTAAGCCACTTGGCCCAAGGCCACACAGCC 31099
> 1564 AG 1565
> 31098 AG 31097

RESULT 26
IS-09-328-111-672/c
Sequence 672, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Dertli, Adrian
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 672
LENGTH: 377
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(377)
OTHER INFORMATION: n = A,T,C or G

IS-09-328-111-672
Query Match 2.2%; Score 39.2; DB 3; Length 377;
Best Local Similarity 78.3%; Pred. No. 0.082;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

> 1508 AGATGAGAACTGAGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
> 180 AGATGAGAACTGAGGTTTCAGAGAGGCACTTGCTTGGCCCAAGTCTACACAGCGGGGA 121

RESULT 27
IS-08-467-155A-2/c
Sequence 2, Application US/08467155A
Patent No. 5736377
GENERAL INFORMATION:
APPLICANT: Band, Vimla
TITLE OF INVENTION: NES-1 POLYPEPTIDES, DNA, AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

IS-08-467-155A-2
Query Match 2.2%; Score 39.2; DB 1; Length 1454;
Best Local Similarity 78.3%; Pred. No. 0.17;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

> 1508 AGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
> 1292 AGATGAGAACTGAGGTTTCAGAGAGGCACTTGCTTGGCCCAAGTCTACACAGCGGGGA 1233

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-467-155A-2

Query Match 2.2%; Score 39.2; DB 1; Length 1454;
Best Local Similarity 78.3%; Pred. No. 0.17;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

> 1508 AGATGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAA 1567
> 1292 AGATGAGAACTGAGGTTTCAGAGAGGCACTTGCTTGGCCCAAGTCTACACAGCGGGGA 1233

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,155A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/100002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-467-155A-2

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; NUMBER OF SEQUENC

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO. 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
S-08-232-463-14

Query Match 2.2%; Score 39.2; DB 1; Length 7218;
Best Local Similarity 7.0%; Pred. No. 0.43;
Matches 29; Conservative 201; Mismatches 184; Indels 0; Gaps 0;

490 TTTTCCATGGGAGAGATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGCCACAG 549
b 997 TTTTCTCGTTGCCATGCTACGACAGATTAATTCGAGCTGGCTGCGAGTGGAGG 1056
y 550 GCGTATGATGCTGCGCTGATCTGCTGATGAGGCGGCCCATGAGTGTGTTACGCC 609
b 1057 AGCTTGCATTT 1116
y 610 TCACATGTCGCGCTGTCACTGCGCCCGAGCTGTGAGGAGCCACAGAAAGCTGTCCA 569
b 1117 YY 1176
y 670 AGTGTGTGAACCTCACATCCCTCTGAGCTCCGGCCGCCACAAAGTCCTGCCAGACA 729
b 1177 YY 1236
y 730 ACGGACCATGTACACACGAGAGATCTCAGTGCCCATGAGTGTCCCTCCGCC 789
b 1237 YY 1296
y 790 TGCCCAACCATGTGCTCTGCGAGTGCACAGAGGCGCCAGATCTACTGCGGCTCACA 849
b 1297 YY 1356
y 850 CTGCGCCGACAGGCTGCCAGACACCTCCGCTGCCAGACTCTGCTGCC 903
b 1357 YY 1410

RESULT 22
US-09-740-027-3/C
Sequence 3, Application US/09740027
Patent No. 6485939
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001052
CURRENT APPLICATION NUMBER: US/09/740,027
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 24707
TYPE: DNA
ORGANISM: Human

US-09-740-027-3

Query Match 2.2%; Score 39.2; DB 4; Length 24707;
Best Local Similarity 78.3%; Pred. No. 0.85;
Matches 47; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1508 AGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCACACAGCAGAA 1567
Db 13256 AGATGGGAAACTGAGGCTCAGAGATGTGAGGCCCACTGCTGCTGACATCATCACAGCCAGAA 13197

RESULT 33
US-08-343-760A-1
; Sequence 1, Application US/08343760A
; Patent No. 5679783
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M
; APPLICANT: Saeal, Yoshiki
; TITLE OF INVENTION: Tissue Differentiation Affecting
; TITLE OF INVENTION: Factor and Composition
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,760A
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 3100.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 363-5556
; TELEFAX: (415) 362-5418
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3796 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-343-760A-1

Query Match 2.1%; Score 39; DB 1; Length 3796;
Best Local Similarity 65.5%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 594 GTGAGTTGTACCCGCTCCACTGTCCGCTGTCCACTGCGCCGCTGTCAGCTGCGCCAGCGAGCCA 653
Db 2466 GTGATTGTGATCTCTATGTGTGCCCACTCTTGAACTGCTCCCGAGCTCTGCTTCATTGCCA 2525

QY 654 CAGCAATGCTGTCCAAAGTGTGGAA 680
Db 2526 GATCAGTGTGCTCTGTGTGTGAAGAA 2552

RESULT 34
US-08-927-219-130
; Sequence 130, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya

MOLSCULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: Join(3520..3630, 5093..5117, 5210..5347, 5450
LOCATION: ..5584, 8253..8395, 9269..9386, 10515..11102)
US-08-756-506-1
Query Match 2.1%; Score 38.8; DB 2; Length 11725;
Best Local Similarity 58.8%; Pred. No. 0.74;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
2y 1448 CTTTGCCCTGGACACGAGGCTCGGACTTGTGGAGATCTACTCTGGAAGCTGTAA 1507
3095 CTATCTCTGGCCAGGCTGATTGGATGTTTATCATCGGCTCATCCCATGTTTT 3154
2y 1508 AGATGAGGAATCAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAG 1561
3155 GGATGAGTAATGAACTTAGAAGGTAAAGACACTGGCTCAAGGTGCACACAG 3208
RESULT 37
US-08-370-319C-12/c
Sequence 12, Application US/08370319C
Patent No. 5856091
GENERAL INFORMATION:
APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W lfel, Thomas; Coulie, Pierre;
APPLICANT: Boon-Fallieur, Thierry; De Plaeen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: 10-JANUARY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/272,351
FILING DATE: 8-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5856091man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
OTHER INFORMATION: kilobases
US-08-370-319C-12

Query Match 2.1%; Score 38.6; DB 2; Length 4129;
Best Local Similarity 72.5%; Pred. No. 0.47;
Matches 50; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1503 GTAAAGATGAGAACTCAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGC 1562
3342 GTTACAGATGGGAACTGGGGCACAGAGAGGTTAACTCGTTCCTCATGTCACACAAC 3283
Qy 1563 CAGAATCTT 1571
Db 3282 TAGTAAGTT 3274
RESULT 38
US-09-224-834-12/c
Sequence 12, Application US/09224834
Patent No. 6201111
GENERAL INFORMATION:
APPLICANT: Brichard, Vincent; Van Pel, Aline;
APPLICANT: Traversari, Catia; W lfel, Thomas; Coulie, Pierre;
APPLICANT: Boon-Fallieur, Thierry; De Plaeen, Etienne
TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/032,978
FILING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6201111man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 4129 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence is preceded by an
OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
OTHER INFORMATION: kilobases
US-09-224-834-12
Query Match 2.1%; Score 38.6; DB 3; Length 4129;
Best Local Similarity 72.5%; Pred. No. 0.47;
Matches 50; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 1503 GTAAAGATGAGAACTCAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGC 1562
3342 GTTACAGATGGGAACTGGGGCACAGAGAGGTTAACTCGTTCCTCATGTCACACAAC 3283
Db 3342 GTTACAGATGGGAACTGGGGCACAGAGAGGTTAACTCGTTCCTCATGTCACACAAC 3283

Qy 1468 CCTCGACTTGGTGGAGATCTAC-CTCTGGAAGCTGTGTAAGATGAGGAAACTGAGGCT 1526
Db 53459 CACCGCTCCCGCAGTGTAGACGTTCTTATCCCGCCTGGCAGGTGAGGAGACTGATGCT 53400
Qy 1527 CAGAGAGGTGAGTACTCTGGCCCGCAGGCCACACAGCCAGAA 1567
Db 53399 CAGCTGGTTAAGTGCACAGGCACAGGCCACACACCTTAGGA 53359

Search completed: January 31, 2004, 04:01:41
Job time : 120 secs

2y 1563 CAGAACTCTT 1571
Db 3282 TAGTAAGTT 3274

RESULT 39

JS-09-146-053-4/c
; Sequence 4, Application US/09146053A
; Patent No. 6399349
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-4

Query Match 2.1%; Score 38.6; DB 4; Length 50000;
Best Local Similarity 77.0%; Pred.No.1.9;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACTGGCCCAAGSCCAGCAGCC 1563
Db 14773 TAACAGAGGAAAACTGAGCCTCAGAGAGCTGAATAACTTGGCCCAAGSTCAGCAGCT 14714

Qy 1564 A 1564
Db 14713 A 14713

RESULT 40

US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01663
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(111282)
; OTHER INFORMATION: n = A,T,C or G

US-09-754-250-3

Query Match 2.1%; Score 38.6; DB 4; Length 111282;
Best Local Similarity 56.5%; Pred.No.3;
Matches 91; Conservative 0; Mismatches 69; Indels 1; Gaps 1;

Qy 1408 TCCACATCGGTATCCCAAGCCAGACACCTGCGCTTGCCCTGGACACAGG 1467
Db 53519 TCCTGACCTTGTGATCCACCTTGCCCTCCCAAGTGTCTGAGATTACAGCGTGAGC 53460

GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

un on: January 31, 2004, 00:43:14 ; Search time 3965 Seconds
(without alignments)
11137.764 Million cell updates/sec

itle: US-09-890-456-8
erfect score: 1817
equence: 1 ggacataaaaggaacaa.....aagttgcataaccatcaaa 1817

coring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

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inimum DB seq length: 0
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ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST:*

- 1: em_ests:*
- 2: em_esthm:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: gb_est1:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_man:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	790.4	43.5	1047	11 AF332891	AF332891 Homo sapi
2	733.2	40.4	1485	11 AK007577	AK007577 Mus muscu
3	591.4	32.5	601	9 AI739159	AI739159 w18h06.x
4	479.4	26.4	481	13 BX091758	BX091758 BX091758

5	428.2	23.6	545	12 BI774183	BI774183 466194 MA
6	422.4	23.2	756	12 BI112782	BI112782 602898795
7	405.8	22.4	424	9 AL047873	AL047873 DKE2P586M
8	406.8	22.3	768	12 BI113110	BI113110 60289895
9	389.8	21.5	915	10 BE911015	BE911015 601662108
10	380	20.9	391	9 AW083466	AW083466 xc02b12.x
11	379.2	20.9	474	10 BF653749	BF653749 277683 MA
12	340.6	18.7	421	9 AA040433	AA040433 zk46c09.s
13	320.8	17.7	323	9 AI205845	AI205845 gg30f03.x
14	300.4	16.4	629	12 BI067140	BI067140 p81f1p.p0
15	297.4	16.2	352	9 AW482630	AW482630 46339 MAR
16	294.6	15.8	716	10 BF134285	BF134285 601784261
17	287.2	15.4	373	9 AW425392	AW425392 57293 MAR
18	279.2	14.8	398	9 AA042913	AA042913 zk56e08.s
19	269.6	14.8	368	9 AW356676	AW356676 39202 MAR
20	268.6	14.7	667	13 BQ181634	BQ181634 UI-R-EUO-
21	267.8	14.3	348	9 AA037778	AA037778 zk38f06.s
22	259.4	13.8	347	9 AI343625	AI343625 qp1b04.x
23	251.2	13.8	376	9 AV661482	AV661482 AV661482
24	251.2	13.8	452	10 BS629331	BS629331 uu36f11.y
25	250.8	13.7	294	14 CS047807	CS047807 NISC_GJ01
26	249.8	13.7	294	14 CS047808	CS047808 NISC_GJ01
27	249.8	13.7	294	14 CS047809	CS047809 NISC_GJ01
28	224.8	12.4	228	10 BF437134	BF437134 7p63f11.x
29	223.2	12.3	228	10 BF437637	BF437637 7p78405.x
30	220.8	12.2	442	10 BS629653	BS629653 uu36f11.x
31	212.2	11.7	450	12 BI286468	BI286468 UI-R-DE0-
32	205.8	11.3	750	10 BG175998	BG175998 602335223
33	194	10.7	770	10 BF181980	BF181980 601805915
34	191.6	10.5	525	2 HSM070338	HSM070338 Homo sapi
35	190.6	10.5	248	9 AA040432	AA040432 zk46c09.x
36	181.6	10.0	472	9 AA514464	AA514464 nf57f02.s
37	177.6	9.8	275	9 AA042926	AA042926 zk56e08.x
38	175.2	9.6	245	9 AA040904	AA040904 zk38f06.x
39	170.6	9.4	939	13 BU514386	BU514386 AGENCOURT
40	157	8.6	855	10 BS799088	BS799088 601588485
41	155.2	8.5	1201	13 BX381985	BX381985 BX381985
42	154.6	8.5	1201	13 BX381986	BX381986 BX381986
43	153.4	8.4	275	10 BS513170	BS513170 BS513170
44	153.4	8.4	278	9 AV052475	AV052475 AV052475
45	150.4	8.3	971	9 AL559420	AL559420 AL559420

ALIGNMENTS

RESULT 1

AF332891 1047 bp mRNA linear HTC 13-JUL-2001

LOCUS AF332891 Homo sapiens FKSG37 (FKSG37) mRNA, complete cds.

DEFINITION AF332891

ACCESSION AF332891.1 GI:12276190

VERSION AF332891.1

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1047)

AUTHORS Wang, Y.-G. and Gong, L.

TITLE Cloning of FKSG37, a novel gene located on human chromosome 11q14

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1047)

AUTHORS Wang, Y.-G.

TITLE Direct Submission

JOURNAL Submitted (01-JAN-2001) Beijing Fengkesheng Function Gene Technology Ltd., 4 Toutiao Lu Chang Street, Xuanwu District, Beijing 100050, P.R. China

FEATURES

Location/Qualifiers

1..1047

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="11"

1412 CACATCGGTATCCCAAGCCAGACAACCTCGTTCGCTTTGGCTTGGAAACACGAGGCCTC 1471
 Db 801 CACATCGGTATCCCAAGCCAGACAACCTCGTTCGCTTTGGCTTGGAAACACGAGGCCTC 860

1472 GCATCTGGTGGAGATCTACTCTGGAAGCTGTAAGAAG 1509
 Db 861 GCATCTGGTGGAGATCTACTCTGGAAGCTGTAAGAAG 898

RESULT 2
 AK007577 LOCUS linear HTC 05-DEC-2002
 DEFINITION Mus musculus 10 day old male pancreas cDNA, RIKEN full-length
 enriched library, clone:181002C01 product:CHORDIN-RELATED PROTEIN
 NEURALIN-2 homolog [Mus musculus], full insert sequence.

ACCESSION AK007577 GI:12841206
 VERSION 1
 KEYWORDS Mus musculus (house mouse)
 SOURCE HTC; CAP trapper
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Carminci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 93279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carminci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20493974
 PUBMED 11042159

REFERENCE 3
 AUTHORS Konno, H., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carminci, P.,
 Shibata, K., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system -384 format
 sequencing pipeline with 384 multipicillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085560


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VERSION BI112782.1 GI:14563683
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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AUTHORS NIH-MSC http://img.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11080 row: n column: 24
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 424)
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished
COMMENT Contact: Koehler K
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKZP586M2422) is available at the RZPD in Berlin.

```

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES	SOURCE
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2. The number of times the subject has been hospitalized for medical illness.	
3. The number of times the subject has been hospitalized for drug abuse.	
4. The number of times the subject has been hospitalized for criminal behavior.	
5. The number of times the subject has been hospitalized for substance abuse.	
6. The number of times the subject has been hospitalized for mental health problems.	
7. The number of times the subject has been hospitalized for physical health problems.	
8. The number of times the subject has been hospitalized for social problems.	
9. The number of times the subject has been hospitalized for family problems.	
10. The number of times the subject has been hospitalized for work-related problems.	
11. The number of times the subject has been hospitalized for financial problems.	
12. The number of times the subject has been hospitalized for legal problems.	
13. The number of times the subject has been hospitalized for educational problems.	
14. The number of times the subject has been hospitalized for religious problems.	
15. The number of times the subject has been hospitalized for cultural problems.	
16. The number of times the subject has been hospitalized for ethnic problems.	
17. The number of times the subject has been hospitalized for racial problems.	
18. The number of times the subject has been hospitalized for sexual problems.	
19. The number of times the subject has been hospitalized for gender problems.	
20. The number of times the subject has been hospitalized for age-related problems.	
21. The number of times the subject has been hospitalized for disability-related problems.	
22. The number of times the subject has been hospitalized for chronic health conditions.	
23. The number of times the subject has been hospitalized for acute health conditions.	
24. The number of times the subject has been hospitalized for infectious diseases.	
25. The number of times the subject has been hospitalized for autoimmune disorders.	
26. The number of times the subject has been hospitalized for endocrine disorders.	
27. The number of times the subject has been hospitalized for cardiovascular diseases.	
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30. The number of times the subject has been hospitalized for musculoskeletal disorders.	
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41. The number of times the subject has been hospitalized for genetic conditions.	
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AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LLNL at:

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REFERENCE	1	(Bases 1 to 915)	
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Invitrogen Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L1AM9128 row: p column: 01 High quality sequence stop: 743. Location/Qualifiers 1. .915 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:3962352" /tissue_type="tumor, biopsy sample" /dev_stage="10 months, virgin" /lab_host="DH10B" /clone_lib="NCI_CGAP_Mam1" /notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site: 2; Not1; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
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AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI_CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 368. Location/Qualifiers 1. .391 /organism="Homo sapiens"		


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Tel: 402 762 4366
Fax: 402 782 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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        /clone_lib="MARC 3BOV"
        /note="Vector; pcMV SPORTr6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
BASE COUNT      137 a   124 c   118 g       95 t
ORIGIN
Query Match          20.9%; Score 379.2; DB 10; Length 474;
Best Local Similarity 89.0%; Pred No. 4,7e-89;
Matches 422; Conservative 0; Mismatches 48; Indels 4; Gaps 1;
Qy               1326 ATTGGCCAGAGCAAGAAGCAGACCTCGGCCACAGTGAGATCATGTTCCACAGGTGTCCC 1395
Db                1 ATTGTCTCAGAGCACAGGAGCACTCGGCCACAGTGAGATCATGTTCCACAGGTGTCCG 60
Qy              1386 AAGCGACCGGCGCGGTCTCTGTCACACATCGGTATTCGCCAAGCCCCAGACMACCTGGGT 1445
Db              61 AAGCGCGCAGGTCAGAGTGTCTGTTCCACAGTCAGTATPCCCCAAGCCCCGGAACAACCTGGGT 120
Qy             1446 GCCTTTGCCCTCGAAACACAGAGGCGCTCGGAGTCTGTGGAGATCTACCTCTGGAAAGCTGGTA 1505
Db            121 GCCTTTGCCCTCGAGCGTGAAGCGCTCTGAGCAGGTGGAGATCTACCTCTGGAAAGCTGGTG 180
Qy           1506 AAAGATCAGAGAAACTGAGGCTCAGAGAGTGGAAGTACCTGGGCCAAGGCCACACAGCCAG 1555
Db          181 AAAGATCAGAGAACTGAGGCTCAGAGAGGTGAAGTACCTGGGCCAAGGCCACACAGCCAG 240
Qy         1566 AATCTTCCACTTGACTCAGATCAAGAAAAGTCAGGAAGAACAGTCTCCAGAAAGAGGCACCA 1625
Db       241 AATCTTCCAATTAA TTCAGATCAAGAAAAGTCAGGAAGAACAGTCTCCAGAAAGAGGCCTCA 300
Qy     1626 GCATCTCCGACTGCTCGCTGGSCCCCGACAGAAAGTCACTGGAAAGTCATCTCTAGCCCCAGAC 1685
Db   301 GAATCTTCGGCTGCTCAGCGCACCCAGAAAGTCACTGGAAAGTCACTCTAGCCCCAGAC 360
Qy 1686 CTTGGAGCTGAAGSTCAGGCGCAGGCTCCAGACAAAGTGCACCAAGTGCACCAAGATCAAAGA---C 1741
Db 361 CCCGGAGCTGAAGSTCAGGCTCAGCGCCAGTCCAGCAANAATGACCAAGACCTTATAACAAGATC 420
Qy 1742 CTACAGTTGCAGATATGACTGCTATATGCTTATCTGTTATATATATATATATATATAT 1795
Db 421 TGAACAGTTGCAGATATGAGCTTTATCATTTTTTGTGTTATATATATATATATAT 474

RESULT 12
AA040433/c
LOCUS
DEFINITION zk46c09.s1 Soares_pregnant_uterus_NDHFU Homo sapiens cdna clone IMAGE:485872 3', mRNA sequence.
ACCESSION AA040433
VERSION AA040433.1 GI:1516711
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 421)

Hillier, L., Lennon, G., Becker, M., Bernaldo, M.F., Chiapelli, B., Chissee, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Marling, T., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevas, B., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

97044478

JOURNAL PUMED COMMENT

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewartson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1346 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 341.

FEATURES

Location/Qualifiers

1..421

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:13759586"

/db_xref="taxon:9606"

/clone="IMAGE:495872"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares pregnant uterus NHPU"

/note="Organ: uterus; Vector: pT73-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGATTCGGCGCGCGCTTTTCTTTTCTTTT 3', double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bernaldo."

BASE COUNT

81 a 95 c 111 g 130 t 4 others

ORIGIN

Query Match 18.7%; Score 340.6; DB 9; Length 421; Best Local Similarity 96.4%; Pred. No. 7.3e-79; Matches 370; Conservative 0; Mismatches 10; Indels 4; Gaps 2;

QY 1437 AACCTGGCTGCTTGGCTGGACAC--GAGCGCTGGAGTCTGGTGGAGTCTACCTC 1493

DB 383 AACCTNCTGCTTTCCTTCCCTGGGACACGAGGCTCGGACTTGGTGGAGTCTACCTC 324

QY 1494 TGGAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGGCTGAGTACCTGCGCCCAAG 1553

DB 323 TGGAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGGCTGAGTACCTG-CCNAG 265

QY 1554 CCACACAGCCAGAACTTCCACTTGAATCAGATCAAGAAAGTCAGAGCAAGACTTCCA 1613

DB 264 CCACACAGCCAGAACTTCCACTTGAATCAGATCAAGAAAGTCAGAGCAAGACTTCCA 205

QY 1614 GAAAGGCGCAGCACTTCCGACTCTCGTGGCCCCCAGCAAGGTCACTGGAACTCTT 1673

DB 204 GAAAGGCGCAGCACTTCCGACTCTCGTGGCCCCCAGCAAGGTCACTGGAACTCTT 145

QY 1674 CCGAGCCAGCCCTGGAGCTCAGGCTCAGGCGGCTGAGTACCTGAGCAAGTACCAAGACATA 1733

DB 144 CCGAGCCAGCCCTGGAGCTCAGGCTCAGGCGGCTGAGTACCTGAGCAAGTACCAAGACATA 85

QY 1734 ACAAGACCTAACAGTTGGAGATATGAGCTGATTAATTTGTTATTATATATATAA 1793

Db 84 ACAAGACCTAACAGTTGGAGATATGAGCTGATTAATTTGTTATTATATATAA 25

QY 1794 TAAGAAGTTGCATTAACCATCAAAA 1817

DB 24 TAAGAAGTTGCATTAACCATCAAAA 1

RESULT 13

LOCUS A1205645/c

DEFINITION QG30G03.x1 Soares Testis NHT Homo sapiens cDNA clone IMAGE:1836724 3', similar to gb:XS7025.fna1 INSULIN-LIKE GROWTH FACTOR IA

ACCESSION A1205645

VERSION A1205645.1

KEYWORDS GI:3764317

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 329)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: rgs@bbs-rcmail.nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio-llnl.gov/bbrp/image/image.html Insert length: 982 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 318.

FEATURES

Location/Qualifiers

1..329

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1836724"

/sex="male"

/lab_host="DH10B"

/clone_lib="Soares testis NHT"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTACCAATCGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3', Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT

63 a 75 c 77 g 114 t

ORIGIN

Query Match 17.7%; Score 320.8; DB 9; Length 329; Best Local Similarity 99.4%; Pred. No. 1.1e-73; Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1494 TGGAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGGCTGAGTACCTGCGCCCAAG 1553

DB 329 TGGAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGGCTGAGTACCTGCGCCCAAG 270

QY 1554 CCACACAGCCAGAACTTCCACTTGAATCAGATCAAGAAAGTCAGAGCAAGACTTCCA 1613

DB 269 CCACACAGCCAGAACTTCCACTTGAATCAGATCAAGAAAGTCAGAGCAAGACTTCCA 210

QY 1614 GAAAGGCGCAGCACTTCCGACTCTCGTGGCCCCCAGCAAGGTCACTGGAACTCTT 1673

b 209 GAAAGGACAGCACTTCGACTGCTGCTGGCCCCCAGCAAGGTCACTCGAAGCTCTT 150

y 1674 CTTAGCCAGACCTCTGGAGCTGAAGTTCACGGCCAGTCCAGCAAAAGTGACCAAGACATA 1733

b 149 CTTAGCCAGACCTCTGGAGCTGAAGTTCACGGCCAGTCCAGCAAAAGTGACCAAGACATA 90

y 1734 ACAAGACCTAACAGTTGTCAGATGAGCTGTATTAATTTGTTATTATATATTAATAAAA 1793

b 89 ACAAGACCTAACAGTTGTCAGATGAGCTGTATTAATTTGTTATTATATATTAATAAAA 30

y 1794 TAAGAGTTGCATAACCATCAAAA 1817

b 29 TAAGAGTTGCATTACCTCANA 6

RESULT 14

LOCUS BI067140 629 bp mRNA linear EST 15-JUN-2001

DEFINITION pgfin.pk010.n11 normalized chicken fat cDNA library Gallus gallus

CCESION (BC002909) Similar to chordin-like [Homo sapiens], mRNA sequence.

ERSON BI067140

EWORDS BI067140.1 GI:14474662

OURCE EST.

ORGANISM Gallus gallus (chicken)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS 1 (bases 1 to 629)

TITLE Cogburn, L.A., Morgan, R.W. and Burnside, J.

JOURNAL Chicken ESTs from fat

COMMENT Unpublished

Contact: Larry A. Cogburn

University of Delaware

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1335

Fax: 302-831-2822

Email: cogburn@udel.edu, www.chickest.udel.edu.

EATUES source

1. 629

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="pgfin.pk010.n11"

/sex="Male and Female"

/tissue types="fat"

/lab host="E.coli EMDH10B"

/clone lib="normalized chicken fat cDNA library"

/note="Vector: pSPORT1"

ASE COUNT 142 a 191 c 167 g 120 t 9 others

RIGIN

Query Match 16.5%; Score 300.4; DB 12; Length 629;

Best Local Similarity 69.8%; Pred No. 3.8e-69;

Matches 417; Conservative 0; Mismatches 179; Indels 1; Gaps 1;

y 639 CTGTGACGGAGCCACAGCAAGTGTCTCCCAAGTGTGTGAACCTTCACATCTCCCTTGGGA 698

b 2 CCGGTACAGACCCCAAGAGTGTCTCCCAAGTGTGTGTGACCAAAATTCCTCTTGGT 61

y 699 CTCGGGGCCCAACCAAGTCTCTGCCAGCACCAACGGGACCATGTATACCAACAGGAGATC 758

b 62 CTCGGGGCACTGTCTGAGTCTCTGCCAGTACAAATGGGACGACGTACCAGAGGAGATG 121

y 759 TTCAGTGGCCATGAGCTGTTCCTCCCTGGCTGCCCAACAGTGTCTCTGCAAGTGC 818

b 122 TTCACCAACCATGAGCTCTTCCAGAGCCGAGCCCAACAGTGTGTGAGTGCAGTGC 181

y 819 ACAGAGGGCCAGATCTACTGGGCTTCACACTCTGCCCAACAGGTCGCCAGACCC 878

b 182 TCTGAAGGCCAGATTACTGTGGCTTGGTACCTGCCAGAGCTGTGTGCTCAATCCC 241

Qy 879 CTCCCGTGCAGACTCTCTGCTGCCAAGCTTGCAAGATGAGGCAAGTGCATCGATCGAT 938

Db 242 CTTAAACCGTGCAGACTCTCTGCTGCCAAGCTTGCAAGATGAGGCTCATATGAGAAGTCTGCG 301

Qy 939 GAAGAGGACACTGTGCAGTGCCTCCATCGGGTGAGACATCTCAGAGTCCATGTTCAGT 998

Db 302 GAAGAGGAAACCCCTGCAGTTAAACAGAGGTGTAGGCACTCAACAAGACCATGCTTGCGG 361

Qy 999 GATGTGTGGAGAAAGAGAGCCCGGGCCACCCAGCCCTGCTGCTGCTGCTGCTGCTGCTG 1058

Db 362 GAAGCAATGTGGCAAGAGCCACCGGAGCCACCGGCTGCCACCATGCTCAGTTCCTCACTG 421

Qy 1059 AGCTTCATCTCCCTGCCACTTCAGACCCAGGGAGC-AGCAGCAACAATGTCAAGATCGT 1117

Db 422 GAGTTCACTCCCGAGGCTTCAACCCAGGGNNAGGTGGCCACCTGTGAAGATCGT 481

Qy 1118 CTTGAAGAGAGAAACATGAAGAAAGCTGTGTGCAATGGCGGAGAGCTACTCCACGGGGA 1177

Db 482 CTTGAAGAGAGAACACAGAAAGCTGTGTGTACAAATGGGAAGACTACTCCCATGGAGA 541

Qy 1178 GGTGTGGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234

Db 542 AGTGTGGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598

RESULT 15

LOCUS BI456773 942 bp mRNA linear EST 21-AUG-2001

DEFINITION 603174663f1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5254095 5', mRNA sequence.

ACCESSION BI456773

VERSION BI456773.1

KEYWORDS GI:15247429

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 942)

TITLE NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11641 row: n column: 16

High quality sequence start: 2

High quality sequence stop: 833.

High quality sequence stop: 833.

Location/Qualifiers

1. 942

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:5254095"

/tissue_type="tumor, gross tissue"

/dev stage="7 months"

/lab host="DH10B"

/clone lib="NCI CGAP Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; Site 2: NCI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 204 a 294 c 226 g 218 t

ORIGIN

Query Match 16.4%; Score 297.4; DB 12; Length 942;

Best Local Similarity 70.3%; Pred. No. 2.8e-67;		Mamm. Genome 13 (8), 475-478 (2002)	
Matches 529; Conservative 0; Mismatches 206; Indels 18; Gaps 9;			
QY 472 GCCAGACATGTTCTGCTTTCATCGGAGAGATATACCCCGGAGAGCTGGAC 531			
DB 185 GCTCGGCAAGTCTGCTTTTCGGTGAAGATATATACCCCGG-AGAGCTGGACC 243			
QY 532 CTTACTTGGAGCCCAAGGCTGTATGTAATCTGCTGGCTGTACTCTCAGAGGGGCC 591			
DB 244 CTTACTTGGAGCCCAAGGCTGTATGTAATCTGCTGGCTGTACTCTCAGAGGGGCC 303			
QY 592 ATGTGAGTGTGTTACCGCTTCCACTGTGCGCTGTCCACTGCGCCACGCTGTGACGGAGC 651			
DB 304 ATGTGAATGTGTTACCGCTTCCCGCTG-CCACCCCTTCACGTCTACAGCCCTGTGATGGAGC 362			
QY 652 CACAGCAATGTGTTCCCAAGTGTGGAACCTCACATCTCCTTGGACTCCGGGGCCAC 711			
DB 363 CACAGCAATGTGTTCCCAAGTGTGGAATCTCATCTGCTCTTGGCTCCGAGTTCC 422			
QY 712 CAAAGTCTGTCAGACACAAAGGACCATGTATCAACACGAGAGATCTTCAGTGGCCATG 771			
DB 423 TAAAGTCTGTCAGCTCAATGAGACCAATACCAACATGAGAGATCTTCAGTGGCCAGG 482			
QY 772 AGCTGTTCCTCCCGCTGCCAACACAGTGTGCTCTGCACTGACAGAGGCGCAGA 831			
DB 483 AGCTGTTCCTCCCGCTGCCAACACAGTGTGCTCTGCACTGATGATTGAAGGCCACA 542			
QY 832 TCTACTGCGCTCACACACTGCGCCGAACAGGCTGCCACAGCCCTCCCGCTGCCAG 891			
DB 543 CTTACTGTGCTCATGACACTGTCTGAAACAGCTGCC---CACAACTCCCTCTGGCTG 599			
QY 892 ACTCTGTCGCAAGCTGCAAGATGAGGAGTGAAGCAATCGGATGAGAGGACAGTG 951			
DB 600 ATTCTGCTGTGACAGCTGCAAGACAGGACACTGAGATTCACAGAGAAAACCTTG 659			
QY 952 TGAAGTGTGCTC---CATGGGAGTGAATCTCAGG--ATCATGTTCCAGTGAATCTG 1006			
DB 660 ACACAAAGCTGACATGAGAGAGACATTCACAAAGGAATCCATCTCGAGAGAGACAG 719			
QY 1007 GAGAAAGAGAGCGCCGGGACCCAGCCCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1066			
DB 720 GCGCCAGCAAGCAAGCCCGCCCAACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 779			
QY 1067 CCTGTGCCACTTCAGACCAAGGAGAGGAGCAGACAACTGTCAAGATGCTGCTGAAGA 1126			
DB 780 CATTTCCTCAAGTCAAGTGAAGTGGGGGCGCACAAA---AACCATCAAGATATCTCTG 835			
QY 1127 GAAACATAAGAAACCTGTGCTGATGCGGGAAGAGCTATCTCCAGGAGAGTGTGGCA 1186			
DB 836 CTAACCTTTAAABAGT-TGCCCCCAATGGGAAGACATTT-CCATGGGAGTGTGGCA 893			
QY 1187 CCGGCTTCGCTGCTTGGCCCTTGGCCCTTGGCCCTG 1219			
DB 894 CCC-CATTGTGCTCTTGGCCCCCATGCCCTG 924			
RESULT 16			
AM482630	352 bp	mRNA	linear
LOCUS	46339	MARC	2P1G
DEFINITION	Sus scrofa cdna 5', mRNA sequence.		
ACCESSION	AM482630		
VERSION	AM482630.1	GI:7052736	
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
AUTHORS	1 (bases 1 to 352)		
REFERENCE	Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.		
TITLE	Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly		

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LEM9252 row: j column: 16
 High quality sequence stop: 659.
 Location/Qualifiers
 1..716
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone_image="4012143"
 /tissue_type="tumor, metastatic to mammary"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu30"
 /note="Organ: lung; Vector: pCMV-SPORT6, Site 1: NotI; Site 2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies.
 Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT

152 a 218 c 181 g 165 t
 Query Match 15.8%; Score 287.2; DB 10; Length 716;
 Best Local Similarity 76.3%; Pred. No. 1.2e-64;
 Matches 380; Conservative 0; Mismatches 113; Indels 5; Gaps 2;

472 GCCAGACATGTTCTGCTTTTCATGGGAAGAGATCTCCCGCGGAGAGCTGGCACC 531
 188 GCTCGGGCAAGTGTGCTTTTCGGTGAAGATATATACCCCGCCGAGAGCTGGCACC 247
 532 CCTACTTGAGCCACAGGCGCTGATGTACTGTGCTGCGCTGTACTCTCTCAGAGGCGCCC 591
 248 CCTACTGGAACCAAGGACGATATAGTGGTGGCTGTACTCTCTGAGAATGGAC 307
 592 ATGTGAGTTGTTACCGCTCCACTGTGCGCTGTCCACTGCCCGCCAGCTGTGGGAGC 651
 308 ATGTGAACTGTTACCGCTCGCTGCGGACCCCTTCACTGCTCAGAGCTGTGATGAGC 367
 652 CACAGCAATGCTGTCCCAAGTGTGTGGAACTTCACTCACTCTCTGTGACTCCGGGCCCCAC 711
 368 CACAGCAATGCTGTCCCAAGTGTGTGGAACTTCACTCACTCTGTGACTCCGGGCCCCAC 427
 712 CAAAGTCTCGCCAGCACACGGGACCATGTATACCAACAGGAGAGATCTTTAGTGGCCATG 771
 428 TAAAGTCTCGCCAGCTCAATGAGACACATACCAACATGAGAGAGATCTTTAGTGGCCAGG 487
 772 AGCTGTTCCTCCCGCTGCCAACCAGTGTGCTCTGTGAGCTCCACAGAGGCGCAGA 831
 488 AGCTGTTCCTCCCGCTGCCAACCAGTGTGCTCTGTGAGCTCCACAGAGGCGCAGA 545
 832 TCTACTCGGGCTCAGAACCTGCGCCGAAACAGGCTGCCAGCACCCCTCCCGTGGCAG 891
 546 CTTACTGTGGTCTCATGACCTGTCTTGAACCAATGTGCCAGCAATCTCTCT--TCTG 602
 892 ACTCTGTGTCAGGCTGTGCAAGATGAGGCAAGTGTGAGCAATCGGATGAGAGGACAGT 951
 603 ATTCTGCTGTGAGACCTGTGCAAGAGCAGGACAACTGTGAGCTCCACAGAGAAACTTGA 662
 952 TGCAGTGTGCTTCACTGGG 969
 663 ACCAGGTGAGCATGGG 680

RESULT 18

AW425392 373 bp mRNA linear EST 25-APR-2001
 LOCUS 57293 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION AW425392
 ACCESSION AW425392
 VERSION AW425392.1 GI:6953339
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 1 (bases 1 to 373)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, P., Quackenbush, J. and Keele, J.W.

TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTACGACG
 Plate: 28 row: G column: 24
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

1..373
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NARC 2BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
 85 a 119 c 108 g 61 t

BASE COUNT

ORIGIN

Query Match 15.4%; Score 279.2; DB 9; Length 373;
 Best Local Similarity 84.4%; Pred. No. 1.2e-62;
 Matches 314; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 QY 925 GTGAGCAATCGGATGAGAGAGACAGTGTCCAGTGGCTCCATGGGGTGAGACATCTCTCAGG 984
 Db 2 GTGAGAAGTCGGCTGAGAGAGGACACACACATCACACCAAGGGGTGAACATCCCAAGG 61
 QY 985 ATCCATGTTCCAGTGTGCTGGGAGAGAGAGGCGCGGACCCCGACCCCACTGGCC 1044
 Db 62 ATTGTGTTTCAGGGACAGCGGGAGAGAGAGACTGTAGCACTCCCTGCTCCCACTGGGC 121
 QY 1045 TCAGGCGCCCTCTGAGGCTTATCCCTCGGCACTTCAGACCCCAAGGAGGAGGAGCAGCA 1104
 Db 122 CCAGCGCCCTCTCTGGGGTTCATCCCTCGGCACTTCGACCAAGAGAGGAGGAGGAGCACA 181
 QY 1105 CTGTCAAGATCGTCTCGAAGGAGAAACATGAAGAGAGCTGTGTGCAATGGCGGAGAGCT 1164
 Db 182 CAGTCAAGATTGTTCTGAGAGGAGAAACATGAAGAGAGCTGTGTGCAATGGCGGAGAGCAT 241
 QY 1165 ACTCCACGGGAGGTGTGGCACC CGGCTTCGCTGCTTCGCGCCCTTCGCTGCATCC 1224

[illegible]

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissee, S., Dietrich, N., Duboue, T., Favellio, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Franke, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Warra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)

TITLE 97044478

JOURNAL 8889549

MEDLINE 8889549

PUBMED 8889549

COMMENT Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1272 Std Error: 0.00
Seq primer: -40M13 fwd. from AmerSham
High quality sequence stop: 225.
Location/Qualifiers
1. 348
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/db_xref="taxon:9606"
/clone="IMAGE:485123"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant_uterus_NbHPU"
/notes="Organ: uterus; Vector: p7733-Pac; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7733 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo." 99 t

BASE COUNT 69 a 86 c 87 g 99 t 7 others

ORIGIN

Query Match 14.3%; Score 259.4; DB 9; Length 348;
Best Local Similarity 89.1%; Pred. No. 28-57;
Matches 310; Conservative 0; Mismatches 33; Indels 5; Gaps 3;

Qy 1439 CCTGGTGGCTTTGCCCTGGAAACAGAGGCTCGACTTGGTGGAGATCTACTCT---G 1495
Db 348 CTTGGTGGCTTTGCCCTGGAAACAGAGGCTCGACTTGGTGGAGATCTACTCTATGG 289

Qy 1496 GAAGCTGTTAAAGATGAGGAAC--TGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGC 1554
Db 288 AAGCCTGTTAAAGATGAGGAACCTTGAGGCTCAGAGAGGTGAAGTACCTGGCAAGC 229

Qy 1555 CACAGCCAGATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTT--CCA 1613
Db 228 CACAGCCAGATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCCA 169

Qy 1614 GAAAGAGCAGACACTTGGACTCTGCTGCTGGCCCGCCAGAGTCACTGGAAAGCTTT 1673
Db 168 GAAAGAGNACAGACACTTGGACTCTGCTGCTGGCCCGCCAGAGTCACTGGAAAGCTTT 109

Qy 1674 CTTAGCCCAACCTGGAGTCAAGGTCA CGGCCAGTTCAGACAAAGTGACCAAGACATA 1733
Db 108 CTTAGCCCAACCTGGAGTCAAGGTCA CGGCCAGTTCAGACAAAGTGACCAAGACATA 49

Qy 1734 ACAAGAGCTAACAGTTGAGATATGAGCTGTATATTTGTTATTA 1781
Db 48 ACAAGAGCTAACAGTTGAGATATGAGCTGTATATTTGTTATTA 1

FEATURES source

1. 347
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/clone_lib="NCI CGAP_Kids"
/notes="Organ: kidney; Vector: p7733D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGCGCCGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7733 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo." 120 t

BASE COUNT 62 a 87 c 78 g 120 t

ORIGIN

Query Match 13.8%; Score 251.2; DB 9; Length 347;
Best Local Similarity 93.6%; Pred. No. 38-55;
Matches 262; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1538 AGTACTGGCCCGCCAGGCCACAGCAGCACTTCCGACTGCTGGCCGCCCAAG 1597
Db 280 AGGAGCTGCGGGAAGGGGAATGACAGGGGAATCTTCACCTGACTCAGATCAAGAAAGTCA 221

Qy 1598 GGAAGCAAGACTTCCAGAAAGAGGACAGCACTTCCGACTGCTGGCCGCCCAAG 1657
Db 220 GGAAGCAAGACTTCCAGAAAGAGGACAGCACTTCCGACTGCTGGCCGCCCAAG 161

Qy 1658 GTCACTGGAGCTTCTTAGCCAGACCCCTGGAGCTGAAGCTCAGCGCAGTCCAGACA 1717
Db 160 GTCACTGGAGCTTCTTAGCCAGACCCCTGGAGCTGAAGCTCAGCGCAGTCCAGACA 101

Qy 1718 AAGTGA CCAAGACATTAACAAGACCTTAACAGTTGAGATGAGCTGTATATTTGTT 1777
Db 100 AAGTGA CCAAGACATTAACAAGACCTTAACAGTTGAGATGAGCTGTATATTTGTT 41

Qy 1778 ATTATATATTAATAAATAGAGTTGCAATACCATCAAAA 1817
Db 40 ATTATATATTAATAAATAGAGTTGCAATACCATCAAAA 1

LOCUS AI343625/c

DEFINITION gp1lb04.x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1917679 3', mRNA sequence.

ACCESSION AI343625

VERSION AI343625.1 GI:4080831

KEYWORDS EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 347)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: ccapbs@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D.
CNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers
1. 347
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/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Kids"
/notes="Organ: kidney; Vector: p7733D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGCGCCGCAATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7733 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo." 120 t


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RESULT 24
LOCUS AV661482 376 bp mRNA linear EST 16-JAN-2002
DEFINITION AV661482 GLC Homo sapiens cDNA clone GLC5H06 3', mRNA sequence.
ACCESSION AV661482
VERSION AV661482.1 GI:9882496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 376)
AUTHORS Xiao H., Qu J., Liu F., Huang Q., Cheng Z., Li N., Du J., Hu W., Shen K., Lu G., Fu G., Zhong M., Xu S., Gu W., Huang W., Zhao X., Hu G., Gu J., Chen Z., and Han Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
MEDLINE 21625106
PUBMED 11752456
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..376
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLC5H06"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 127 a 87 c 96 g 66 t
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Best Local Similarity 93.6%; Pred. No. 3.1e-55;
Matches 262; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Y 1538 AGTACCTGGCCCAAGGCCACACAGCCAGAACTCTTCCACTTGAATCAGATCAAGAAAGTCA 1597
b 56 AGGACGTCAGGGAAGGGGAATGACAGGGAATCTTCCACTGACTCAGATCAAGAAAGTCA 115
Y 1598 GGAAGCAAGACTTCAGAAAGAGGACACACTTCCAGCTGCTCGTGGCCGCCCAAG 1657
b 116 GGAAGCAAGACTTCGAAAGAGGACACACTTCCGACTCTGCTCGTGGCCGCCCAAG 175
Y 1658 GTCACTGGAAAGCTCTTCTGAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAGTCAACA 1717
b 176 GTCACTGGAAAGCTCTTCTGAGCCAGACCCCTGGAGCTGAAGGTCAAGGCCAGTCAACA 235
Y 1718 AAGTGAACCAAGACATAACAAGACCTAACAGTTCGAGATATGAGCTGTATATTTGTTT 1777
b 236 AAGTGAACCAAGACATAACAAGACCTAACAGTTCGAGATATGAGCTGTATATTTGTTT 295
Y 1778 ATTATATATTAATAAAGAGTTGCATAACCAATCAAAA 1817
b 296 ATTATATATTAATAAAGAGTTGCATAACCAATCAAAA 335
RESULT 25
LOCUS BE629331 452 bp mRNA linear EST 25-AUG-2000
DEFINITION BE629331 Y1 Soares mammary_gland NMLMG Mus musculus cDNA clone
ACCESSION BE629331
VERSION BE629331.1 GI:9912019
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 452)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1093665
Seq primer: -40RP from Gibco.
FEATURES
source
1..452
location/Qualifiers
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/clone_lib="Soares mammary gland NMLMG"
/note="Vector: p713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p713 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 113 a 153 c 101 g 85 t
ORIGIN
Query Match 13.8%; Score 250.8; DB 10; Length 452;
Best Local Similarity 73.3%; Pred. No. 4.3e-55;
Matches 340; Conservative 0; Mismatches 112; Indels 12; Gaps 1;
Y 825 GGCAGATCTACTGGCGCTCAACACTGCCCCGAAACGAGCTGCCAGACACCTCCCG 884
b 1 GGCCACACTTACTGTGTCTCTCATGACCTGTCTGAAACCCAGCTGCCACCACTCCCT 60
Y 885 CTGCCAGACTCTCTCTCCAGCTGCAAGATGAGCAAGTGAATCGATGAAGAG 944
b 61 CTSCCTGATTCTCTGTGACACTGCAAGACAGCAACTGAGAGTTCCACAGAGAA 120
Y 945 GACAGTGTGAGTGTCTCCATGGGTGAGACATCTCAGGATCCATGTTCCAGTGTCT 1004
b 121 AACTTGACACAGCTGCAGCATGGAGAGACATTTCCAGGATTCATGCTC----- 170
Y 1005 GGGAGAAAGAGAGCGCGGACCCAGCCGCCCTGAGCTCAGCCCTCTGAGCTTC 1064
b 171 --GGAGAGGAGAGGCGCCCAAGCAGCCAGCCGCCCTCAGCTCAGCTCTGGGCTTC 228
Y 1065 ATCCCTCGCACTTTCAGACCCAAAGGAGACAGGAGCAAACTGTCAAGATGCTCTGAAG 1124
b 229 ATCCCTCGCACTTTCAGAGTGTAGGAATGGGAGACAAACCACTCAAGATTATCTTGAAG 288
Y 1125 GAGAAACATAAGAAAGCTGTGTGCATGCGCGGAAGACGTACTCCCAACGGGAGGTGTGG 1184
b 289 GAGAAACATAAGAAAGCTGTGCACACAAATGGGAAGACATACTCCCACTGGGAGGTGTGG 348
Y 1185 CACCGCGCTTCCTGCTTCGGCCCTTGCCTTCCTATGCTATGCTGAGGTGGC 1244

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Db 349 CACCCCACTGCTCTCCCTTGGCCCATGCCCTGCATCTCTGTGCACATGTATCGATGCG 408
Qy 1245 GCACGAGACTGCCAGGCTGTGACTGCTGCCACCGAGTACCCCTG 1288
Db 409 TACCAGGACTGCCACGCTGTGACCTGCCACCAATATCCCTG 452

RESULT 26
CB047807/c
LOCUS
DEFINITION
3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
cDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LHAM8006 row: C column: 3
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 57 a 59 c 70 g 108 t
ORIGIN
Query Match 13.7%; Score 249.8; DB 14; Length 294;
Best Local Similarity 99.2%; Pred. No. 6.6e-55;
Matches 251; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1565 GAATCTTCCATTCAGCTCAGATCAAGAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 1624
Db 277 GAATCTTCCATTCAGCTCAGATCAAGAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 218
Qy 1625 AGCACTTCGAGTCTCGTGGCCCCCAGGAAGTCACTGGAACTCTTCTAGCCCGA 1684
Db 217 AGCACTTCGAGTCTCGTGGCCCCCAGGAAGTCACTGGAACTCTTCTAGCCCGA 158
Qy 1685 CCTGGAGTGAAGGTCA CGGCGAGTCCAGCAAAAGTGCACCAAGACATAA CAAGACCTA 1744
Db 157 CCTGGAGTGAAGGTCA CGGCGAGTCCAGCAAAAGTGCACCAAGACATAA CAAGACCTA 98

Qy 1745 ACAGTTCAGATATGAGCTGTATTAATTGTTTATTATATTAATAAATGAAGATTGC 1804
Db 97 ACAGTTCAGATATGAGCTGTATTAATTGTTTATTATATTAATAAATGAAGATTGC 38
Qy 1805 ATAACCATCAAAA 1817
Db 37 ATTACCTCAAAA 25

RESULT 27
CB047808
LOCUS
DEFINITION
NISC_GJ01b02.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3270458
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
cDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LHAM8006 row: C column: 3
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..294
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/lab_host="DH10B"
/clone_lib="NCI CGAP Pr28"
/notes="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 70 c 59 g 57 t
ORIGIN
Query Match 13.7%; Score 249.8; DB 14; Length 294;
Best Local Similarity 99.2%; Pred. No. 6.6e-55;
Matches 251; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1565 GAATCTTCCATTCAGCTCAGATCAAGAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 1624
Db 18 GAATCTTCCATTCAGCTCAGATCAAGAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCAC 77
Qy 1625 AGCACTTCGAGTCTCGTGGCCCCCAGGAAGTCACTGGAACTCTTCTAGCCCGA 1684
Db 78 AGCACTTCGAGTCTCGTGGCCCCCAGGAAGTCACTGGAACTCTTCTAGCCCGA 137
Qy 1685 CCTGGAGTGAAGGTCA CGGCGAGTCCAGCAAAAGTGCACCAAGACATAA CAAGACCTA 1744

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>b 138 CCTGGAGCTGAAGGTCACGCCAGTCCAGACAAAGTGACCAAGACATACCAAGACCTA 197
>y 1745 ACAAGTTCAGATGAGCTGTATTAATTTGTTATTATATATATTAATAAAGAGTTGC 1804
>b 198 ACAAGTTCAGATGAGCTGTATTAATTTGTTATTATATATATTAATAAAGAGTTGC 257
>y 1805 ATAACCATCAAAA 1817
>b 258 ATTACCCCTCAAAA 270

RESULT 28
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DEFINITION 7p8d05.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3650469 3'
similar to TR:Q9UGL7 09UGL7 HYPOTHETICAL 21.1 KD PROTEIN ;, mRNA
sequence.
ACCESSION BF437134
VERSION BF437134.1 GI:11449466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
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/clone="IMAGE:3650469"
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/lab_host="DH103"
/clone_lib="NCI CGAP Pr28"
/note="Organ: Prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonesIDs
985608-986759, 110192-110199, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 47 a 49 c 55 g 77 t
ORIGIN
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Best Local Similarity 99.1%; Pred. No. 2.4e-48;
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

>y 1590 GAAAGTCAGAGACAGACTTCCAGAAAGGACACAGACTTCGAGCTGCTGCGCC 1649
>b 228 GAAAGTCAGAGACAGACTTCCAGAAAGGACACAGACTTCGAGCTGCTGCGCC 169
>y 1650 CCACGAGGTCACCTGGAACGCTCTTCTAGCCAGACCTCGAGCTGAAGGTCA CGGCCAG 1709
>b 168 CCACGAGGTCACCTGGAACGCTCTTCTAGCCAGACCTCGAGCTGAAGGTCA CGGCCAG 109

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>y 1710 TCCAGACAAAGTGACCAAGACATACCAAGACCTAACAGTTGCAGATATGAGCTATAA 1769
>b 108 TCCAGACAAAGTGACCAAGACATACCAAGACCTAACAGTTGCAGATATGAGCTATAA 49
>y 1770 TTGTGTTATTATATATTAATAAATAAGAAAGTTGCATAACCATCAAAA 1817
>b 48 TTGTGTTATTATATATTAATAAATAAGAAAGTTGCATTACCCCTCAAAA 1

RESULT 29
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DEFINITION 7p78d05.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3651896 3'
similar to TR:Q9UGL7 09UGL7 HYPOTHETICAL 21.1 KD PROTEIN ;, mRNA
sequence.
ACCESSION BF437637
VERSION BF437637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 228)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoimage.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..228
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/clone_lib="NCI CGAP Pr28"
/note="Organ: Prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonesIDs
985608-986759, 110192-110199, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 47 a 50 c 55 g 76 t
ORIGIN
Query Match 12.3%; Score 223.2; DB 10; Length 228;
Best Local Similarity 98.7%; Pred. No. 6.4e-48;
Matches 225; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

>y 1590 GAAAGTCAGAGACAGACTTCCAGAAAGGACACAGACTTCGAGCTGCTGCGCC 1649
>b 228 GAAAGTCAGAGACAGACTTCCAGAAAGGACACAGACTTCGAGCTGCTGCGCC 169
>y 1650 CCACGAGGTCACCTGGAACGCTCTTCTAGCCAGACCTCGAGCTGAAGGTCA CGGCCAG 1709
>b 168 CCACGAGGTCACCTGGAACGCTCTTCTAGCCAGACCTCGAGCTGAAGGTCA CGGCCAG 109

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2Y 1710 TCACAGAAAGTGACCAAGACATTAACAAAGACTTAACAGTTTCAGATATGAGCTGTATAA 1769
Db 108 TCACAGAAAGTGACCAAGACATTAACAAAGACTTAACAGTTTCAGATATGAGCTGTATAA 49
2Y 1770 TTGTTGTTATTATATATTATTAATAAAGAAGTTGCAATACCATCAAAA 1817
Db 48 TTGTTGTTATTATATATTATTAATAAAGAAGTTGCAATACCATCAAAA 1
RESULT 30
3E29653/c
LOCUS
DEFINITION
ui36611.x1 Soares mammary gland NMLMG Mus musculus cDNA clone
IMAGE:3374061.3, mRNA sequence.
ACCESSION
VERSION
B629653.1 GI:9912270
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 442)
NCI-CCAG <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Other ESTs: ui36611.y1
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1083665
High quality sequence stop: 433.
Location/Qualifiers
1. 442
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone=IMAGE:3374061"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="VDH10B"
/clone_lib="Soares mammary gland NMLMG"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Botaldo."
BASE COUNT 96 a 108 c 109 g 129 t
ORIGIN
Query Match 12.2%; Score 220.8; DB 10; Length 442;
Best Local Similarity 71.8%; Pred No 3.7e-47;
Matches 346; Conservative 0; Mismatches 77; Indels 59; Gaps 2;
Qy 1320 TCAGATTTGCCAGAGACAAGCAGACCTTGGCCAGTGAATCAGTTCTACCAGG 1379
Db 442 TCAGATTTGCCAGAGACAAGCAGACCTTGGCCAGTGAATCAGTTCTACCAGG 383
Qy 1380 TGTCCCAAGCAGCGGGCTCTCTGTCACACATCGGTATCCCAAGCCCAAGCAAC 1439
Db 382 TGTCCCAAGTACAGCGCCAGTTCCAGGTGTACACGTTGGCATCTCCAAAGCCCAAGCAGC 323
Qy 1440 CTGCGTCTGTTGCTTCCCTGGAACACAGAGCTCCGAGCTTGGTGGAGTCTACCTCTCGAAG 1499
Db 322 CTACACGCTTGTCTGAGCATGAGCTCTTGACCAAGTAGAGATGATACATTGGAAG 263
Qy 1500 CTGGTAAAGTAGGAAGACTGAGCTCAGAGAGTGAAGTACCTGCGCCCAAGCCACAC 1559
Db 262 CTGGTGAAG----- 253

Qy 1560 AGCCAGANTCTTCCACTTCTACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAG 1619
Db 252 ----GAATCTACCACTTTGGTTTCAGATCAAGAGATCAGAGATCAGAGATCAGAGATCAGAGAA 198
Qy 1620 GGCACAGACTTCCGAGCTGCTCGCTGSCCCCAAGAGTCACTGGAACTCTTCTCTAGC 1679
Db 197 GGTCTAGAACTTCCGGCTGCTCACCGSCACCCATGAAGTTACTTGGACCGCTCTTCTAGC 138
Qy 1680 CCAGACCTCGAGCTGAAAGTCCAGCGCCAGTCCAGCAAAAGTCCAGCAAAAGTCCAGCAAAAG 1739
Db 137 CCAGACTCCAGAGCTGAAAGTTACAGCAGCCAGCAAAAGTCCAGCAAAAGTCCAGCAAAAGT 78
Qy 1740 A----CTAACAGTTTCAGATATGAGCTGTATAATTGTTTATATATATATAATAATAAATA 1795
Db 77 AGGACCTAAAGAGTTGCAGATACGAGTTTATGTTGTTTATATATATAATAATAAAGA 18
Qy 1796 AG 1797
Db 17 AG 16
RESULT 31
BI286468/c
LOCUS
DEFINITION
UI-R-DE0-cal-d-09-0-UI.s1 UI-R-DE0 Rattus norvegicus cDNA clone
UI-R-DE0-cal-d-09-0-UI 3', mRNA sequence.
ACCESSION
VERSION
BI286468.1 GI:14941145
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 450)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
97044477
PUBMED
8899548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized cervix library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 38-60, >AT_rich#Low_complexity
Seq primer: M13 Forward
POLYA=yes. Location/Qualifiers
1. 450
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DE0-cal-d-09-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-DE0"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DE0
library is a non-normalized library constructed from rat

cervix tissue. For a detailed description of the library from which this clone was derived, please visit our web site at fatecst.eng.uiowa.edu. The subtraction has been previously described in (Isomaido, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG LIB=UI-R-DEO
TAG TISSUE=cervix
TAG SEQ=GACCA

BASE COUNT 96 a 103 c 108 g 142 t 1 others
ORIGIN

Query Match 11.7%; Score 212.2; DB 12; Length 450;
Best Local Similarity 69.9%; Pred. No. 7e-45;
Matches 344; Conservative 0; Mismatches 89; Indels 59; Gaps 2;

1330 GCCCAGAGACAAAGCAGCCCTGGCCACAGTGAGATCAGTTCTACAGGTGTCCCAAGG 1389
1450 GCCCAGAGATGAGCGGATGACGACGACAGTGGTCAATTCACCCGGTGTCCCAAGG 391
1390 CACCGGCGGGTCTCTGTCCACATCGGTATCCCGACCCAGCAACCTGTGGTGGCT 1449
1390 TACAGGCCAGTTCATCTGTGTACACATTTGGTATCTCCAGGCCAGACAGCTACACCGCT 331
1450 TTGCCCTGGAACAGAGGCCCTCGGACTTGGTGAGATCTACCTCTTGGAGCTGTGTAAGG 1509
1330 TTGCTCTGGAACAGAGGCCCTCTGACAGGTAGAGATGTATCTTGGAGGCTGGTGAAG 271
1510 ATGAGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGATC 1569
270 -----GATC 266
1570 TTCCATTGACTCAGATCAGAAAGTCAGGAAGCAAGCTTCAGAAAGAGCAGCAC 1629
265 TACCATTTGATTCAGATCAGAGAGTCAGGAAGCAAGATTCAGAAAGAGGCTCAGAAC 206
1630 TTCGACTCTGCTGGTGGCCCCACGAAAGTCTCTGGAAGCTTCTTCTAGCCAGACCTG 1689
205 TTCGGGCTCTCA CGGCA CCCATGAAGTTACTGGACCTTCTTCTAGCCAGACTCCA 146
1690 GAGCTGAAGTTCAGGCGCAGTCCAGCAAAAGTGACCAAGACATACAAAGA-----CCTAA 1745
145 GAGTTGAAAGTTACAGCCAGCCAGCAAAAGTGACCAAGACATATAGCAAGGACCTAAA 86
1746 CAGTTCAGATATGAGTGTATTAATTTGTTATATATATATATATATATATATATATAT 1805
85 CAGTTCAGATATGAGTGTATTAATTTGTTATATATATATATATATATATATATATAT 26
1806 TAACCATCAAAA 1817
25 CCTCCTCAAAA 14

RESULT 32
LOCUS BGL175998 750 bp mRNA linear EST 06-FEB-2001
DEFINITION 60235223F2 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4458437 5', mRNA sequence.
ACCESSION BGL175998
VERSION BGL175998.1 GI:12682701
KEYWORDS Esi.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 750)
NTH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10256 row: n column: 06
High quality sequence stop: 645.
Location/Qualifiers
1. .750
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4458437"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DE108"
/clone_lib="NCI_CGAP_Mam1"
/note="Origin: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo di. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 157 a 230 c 177 g 186 t
ORIGIN

Query Match 11.3%; Score 205.8; DB 10; Length 750;
Best Local Similarity 73.8%; Pred. No. 4.3e-43;
Matches 355; Conservative 0; Mismatches 117; Indels 9; Gaps 7;

472 GCCCAGACATGTTCTGGCTTTTCCATGGGAAGATATCTCCCGCGGAGAGCTGGCACC 531
245 GCTCGGGCAAGCTCTGCTTTTCGGTGAAGAATATATACCCCGGCGCAGCTGGCACC 304
532 CCTACTTGGAGCCACAGGCTGATGTACTGCTGGCTGTACTCTCTCAGAGGGCGCCC 591
305 CCTACTTGGAAACCAAGGCCAGATATCTGGTGGCGCTGTACTCTCTGAGAATGGAC 364
592 ATGTGATGTTGTACCGCTCTCACTGTCC--GCCTGTCCACTGCCCGCAGCTGTGACGGAG 650
365 ATGTGAATAGTTACCGCTCTCGCTGACCAACCCCTTCAACTGCTCAGAGCTGTGATGGAG 424
651 --CACAGCAATCTGTCTCCAAAGTGTGTGAACCTCACACTCCCTCT--GCACCTCCGGGCC 708
425 CCCACAGCAATGCTGTCCAGGTGTGTGGATCTCTCATGTCCCTCTGGGCGCTCCGAGTTC 484
709 CACCAAGTCTTG--CAGACACACGGGACCATGTACCAACAGGAGATCTTCAG--TG 765
485 CCTTAAAGTCTCTGACACAGACTCAATGAGACCACTACCAACATGGAGAGATCTTCAGATG 544
766 CCATGAGCTGTTCCTCCCGCTG--CCCAACAGTGTGTCTCTGTGAGTGCACAGA 823
545 CCCAGGAGCTGTTCCTGGCCCGCTGTCAACACAGGTGTGTCTGTGTAGTGTCTTGA 604
824 GGGCCAGATC--TACTTGGGCGCTCACAACCTGCCCGCCGACACAGGCTGCCCGACCCCTCC 882
605 AGGCCAACAACTTACTGTGGTCTCATGACCTGTCTCAACACAGGTGTGTCTGTAGTGAATCC 664
883 CGCTGCCAGACTCTGTCTGCAAGCTGTCAAGATGAGGCAAGTGAAGCAATCGGATGAAG 942
665 CTCTGACTGATTAATCTGTGTGAGACTGCAAGGAGACAAAGTGAAGTTCACAGAG 724
943 A 943
725 A 725

RESULT 33
LOCUS BFL181980 770 bp mRNA linear EST 31-OCT-2000
DEFINITION 601805915F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036802 5', mRNA sequence.
ACCESSION BFL181980
VERSION BFL181980.1 GI:11060122
KEYWORDS EST.

SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE	Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 770)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D. Email: cgaps@emall.nih.gov Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLAM9312 row: n column: 03 High quality sequence stop: 752. Location/Qualifiers
FEATURES	1..770 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:4036802" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DH10B" /clone_lib="NCI CGAP Mams" /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies Investigators Providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
BASE COUNT	228 a 209 c 184 g 149 t
ORIGIN	
Query Match	10.7%; Score 194; DB 10; Length 770;
Best Local Similarity	69.3%; Pred. No.5.8e-40;
Matches 338; Conservative	0; Mismatches 90; Indels 60; Gaps 3;
QY	1334 AGAGGACAAAGCAGACCCCTGGCCACAGTCAGATCAAGTTCTTACCAAGGTGTCCCAAGGACCC 1393
Db	316 AGAGGACAGAGCCGGAAGATGACCAAGTCAGATCATTTTCCACCCGGTGTCCCAAGGTACC 375
QY	1394 GGCCCGGGTCTCTGTCCACACATCGGTATCCCAAGGCCAGACAACCTGGCTCGCTTTGC 1453
Db	376 AGCCCAAGTTCACAGGTGTACACGTTGGCATCTCCAAAGCCAGACAGCTACACCGCTTTGT 435
QY	1454 CTTGGAAACACGAGCCTCGGACTTGGTGAGATCTACTCTCTGGAAGCTGTGTAAGAATGA 1513
Db	436 CTTGGAGCATGAAGCCCTCTGACCAAGGTAGAGATGTACATTTGGAAGCTGGTGAAG--- 491
QY	1514 GGAAACTGAGGCTCAGAGAGGTGAAGTACTGTGCCCAAGGCCACAGCAGAGATCTTCC 1573
Db	492 -----GAATCTACC 500
QY	1574 ACTTGACTCAGATCAAGGTCAGGAAGCAGAGCTTCCAGAAAGGACACAGCACTTCC 1633
Db	501 ACTTGTTCAATCAGAGAGTCTAGGAAGCAGAGATTCAGAAAGAGGCTCAGNACTTCC 560
QY	1634 GACTGCTCGCTGGCCCCACAGAGGTCACTGGNAGTCTTCTCTAGCCACAGCCTGGAGC 1693
Db	561 GGCTGCTCACCGGACCCCATGAAGGTTACTTGGACCGTCTTCTAGCCCAAGTCTCCAGNC 620
QY	1694 TGAAGGTCAAGGCCAGTCCAGACAAAGTGACCAAGATACAAAGA-----CTTACAGT 1749
Db	621 TGAAGGTTACAGCCAGCCAGCAAGGTGACCAAGACATTATAGCAAGA CTTAAGAGT 680
QY	1750 TGCAGATATGAGCTGTATTAATTTGTTTATATATATATTAATTAATTAAGAGGTGCATAAC 1809
Db	681 TGCAGATA CGAGTTTATAGTTT--TCGCTTATATATATTTACTCAAGAGTTCGATTTACCGTC 739

2Y 604 ACCGCTCCACTGTCCGCTCTGCACTGCCCCAGCCTGTGACGGACGACGAGATGC 662
|||||
Db 467 ACCGCTCCACTGTCCGCTCTGCACTGCCCCAGCCTGTGACGGACGACGAGATGC 525
|||||

RESULT 35
AA040432 248 bp mRNA linear EST 10-MAY-1997
LOCUS zk46c09.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA clone
DEFINITION IMAGE:485872 5', similar to contains element PTR5 repetitive element
; mRNA sequence.

ACCESSION
VERSION AA040432.1 GI:1516710
KEYWORDS Homo sapiens (human)
SOURCE EST.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Hillier, L., Lennon, G., Becker, M., Donald, M.F., Chiapelli, B.,
Chissey, S., Dietrich, N., Duboue, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lucy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenger, K., Soares, M.B., Tan, F., Thierly-Meg, J., Trevisakis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE 97044478
JOURNAL
MEDLINE
PUBMED 8889549

COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estwatson.wustl.edu
This clone is available royalty-free through LLM; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1346 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 239.

FEATURES
Location/Qualifiers
1..248
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3759586"
/db_xref="taxon:9606"
/clone="IMAGE:485872"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares_pregnant uterus NBHPU"
/note="Organ: uterus; Vector: pT73-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5',
AATCGAAGATTCGGCGCGCTTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

BASE COUNT 49 a 84 c 62 g 46 t 7 others

Query Match 10.5%; Score 190.6; DB 9; Length 248;
Best Local Similarity 95.0%; Pred. No. 2.8e-39;
Matches 207; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

2Y 638 GCCTGTGACGGAGCCACAGCAATCTCTGCCAAGTGTGTGGAACTCACATCCCTCTGG 697
|||||

Db 31 GCAGGTAGTGAGCCACAGCAATCTCTGCCAAGTGTGTGGAACTCACATCCCTCTTT 90
|||||

2Y 698 ACTCCGGGCCCCACCAAGTCTCCAGACACACGGGACCATGTACCAACGGAGAT 757
|||||

Db 91 ACTCCGGGCCCCACCAAGTCTCTCCAGACACACGGGACCATGTACCAACGGAGAT 150
|||||

QY 758 CTTCACTGCGCATGAGCTGTTCCTCTCC- GCCTGCCCAACCACTGTGCTCTGAGCT 816
|||||

Db 151 CTTCACTGCGCATGAGCTGTTCCTCTCC- GCCTGCCCAACCACTGTGCTCTGAGCT 210
|||||

QY 817 GCACAGAGGCCAGATCTACTCTGGGCTCACAACCTGC 854
|||||

Db 211 GCACAGAGGCCAGATCTACTCTGGGCTCACAACCTGC 248
|||||

RESULT 36
AA514464 472 bp mRNA linear EST 18-AUG-1997
LOCUS nf57f02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:924027 3',
DEFINITION mRNA sequence.

ACCESSION
VERSION AA514464.1 GI:2254064
KEYWORDS Homo sapiens (human)
SOURCE EST.
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Straubeberg, Ph.D.
Email: sgabbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 778 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 472.

FEATURES
Location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:924027"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH108"
/clone_lib="NCI_CGAP Co3"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo (dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."

BASE COUNT 97 a 145 c 127 g 103 t

Query Match 10.0%; Score 181.6; DB 9; Length 472;
Best Local Similarity 97.9%; Pred. No. 8.9e-37;
Matches 184; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1327 TTTGCCCGACAGACAAAGACAGCCCTGGCCACAGTGAGATCAGTTCTACAGGTGCCA 1386
|||||

Db 47 TCTCTCCAGAGACAAAGACAGCCCTGGCCACAGTGAGATCAGTTCTACAGGTGCCA 106
|||||

QY 1387 AGGCACCGGGCGGTCTCTGTCACACATCGGTATCCCAAGCCAGACACACCTGGCTC 1446
|||||

Db 107 AGGCACCGGGCGGTCTCTGTCACACATCGGTATCCCAAGCCAGACACACCTGGCTC 166
|||||

```

QY      1447  GCTTTGCTGGACACAGAGCCCTCGACCTTGTGTGAGATCTACCTCTGGAAGCTGGTAA 1506
      |||||||
Db      167  GCTTTGCTGGACACAGAGCCCTCGACCTTGTGTGAGATCTACCTCTGGAAGCTGGTAA 226
      |||||||
QY      1507  AAGGTGAG 1514
      |||||||
Db      227  AAGGTGAG 234
      |||||||

RESULT 37
AA042926
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 275)
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 705 Std Error: 0.00
Seq primer: -28M13 rev2 from Amer sham
High quality sequence stop: 176.
Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3760568"
/db_xref="taxon:9606"
/clone="IMAGE:486854"
/sex="female"
/dev stage="adult"
/lab host="DH10B"
/clone lib="Soares pregnant uterus NbHPU"
/note="Organ: uterus; Vector: p77T3-Pac; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5,
AAGTGGAGAAATTCGGGCGCCCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p77T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
60 a 81 c 75 g 50 t
BASE COUNT
ORIGIN

Query Match 9.8%; Score 177.6; DB 9; Length 275;
Best Local Similarity 88.8%; Pred. No. 8.1e-36;
Matches 245; Conservative 0; Mismatches 22; Indels 9; Gaps 5;

QY      1102  CAACTGTCAAGATCGTCTCGAAGAGAACATAGAAGCTGTGTGATCGCGGAAGA 1161
      |||||||

```

```

Db      1  CAACTGTCAAGATCGTCTCGAAGAGAACATAGAAGCTGTGTGATCGCGGAAGA 60
      |||||||
QY      1162  CGTACTCCCAACGGGAGGT -GTGGACCCGGGCTTCCGTGCTTTCGGCCCTTCGCTGC 1220
      |||||||
Db      61  CGTACTCCCAACGGGAGGTGTGGACCCGGGCTTCCGTGCTTTC -GNCCTTTGCGCTGC 119
      |||||||
QY      1221  ATCCTATGACACCTGTGTGAGATGGCCGCCAGGAC -TGCCAGCGTGTGACCTGTCCACCGA 1279
      |||||||
Db      120  ATCCTATGACACCTGTGTGAGATGGCCGCCAGGACTTGGCCAGCGGTGTGACCTGTCCACCGA 179
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AA040904
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 245)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p77T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

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BASE COUNT 48 a 80 c 66 g 44 t 7 others
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b 210 GCACAGAGGGCCAGATCTACTTGGGGCTCCACAACT 245
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VERSION BUS14386.1 GI:22821912
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE NIH-NGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 939)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M14080 row: m column: 22
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High quality sequence stop: 691.
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256 a 234 c 221 g 228 t

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Db 246 TGTGCTTTGACGCGAGTCAGATGTCCAAGTCTTCATTGCTTTTCAACCGCTGCAATATTC 305
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Db 306 TCATCTCTGTGCTCCCGCTGCCAGACTCTTACCACTGAGTGAACAATAGGTGACCAG 365
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VERSION BE799088.1 GI:10220286
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE NIH-NGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 855)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

BASE COUNT 48 a 80 c 66 g 44 t 7 others
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Query Match 9.4%; Score 170.6; DB 13; Length 939;
Best Local Similarity 52.4%; Pred. No. 9.9e-34;
Matches 408; Conservative 0; Mismatches 359; Indels 12; Gaps 1;
473 CCCAGACATGTTCTGCTTTTCCATGGAAGAGATACCTCCCGGGCAGAGCTGCGACCC 532

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LHM796 row: j column: 22
High quality sequence stop: 831.

FEATURES

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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 215 a 207 c 219 g 214 t
ORIGIN

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Job time : 3973 secs

GenCore version 5.1.6
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Perfect score: 1817
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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11	1338	73.6	1722	6	AX140199	AX140199 Sequence
12	1325	72.9	1722	6	AX140196	AX140196 Sequence
13	1297	71.4	1567	6	AX140204	AX140204 Sequence
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17	1222.8	67.3	1570	6	AX235836	AX235836 Sequence
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20	1121.4	61.7	1515	6	AX140197	AX140197 Sequence
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32	340.6	18.7	421	6	AX337465	AX337465 Sequence
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ALIGNMENTS

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DEFINITION Sequence 8 from Patent WO0134796.
ACCESSION AX140202
VERSION AX140202.1 GI:14280541
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1
Toporoik,A., Biton,S., Savitzky,K. and Bernstein,J.
AUTHORS
TITLE Chordin-like homologue
JOURNAL Patent: WO 0134796-A 8 17-MAY-2001;

RESULT 3

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ACCESSION	AX140203				
VERSION	AX140203.1	GI:14280542			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Toporik, A., Biton, S., Savitzky, K. and Bernstein, J.				
TITLE	Chordin-like homologs				
JOURNAL	Patent: WO 0134796-A 9 17-MAY-2001;				
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source	Location/Qualifiers				
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Best Local Similarity	89.3%; Pred. No. 0;				
Matches 1622; Conservative 0; Mismatches 0; Indels 195; Gaps 1;					
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DB 601	GTTCACGCTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660	1139	----- 1138		
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		1321	GCAAGATTTGCCCGAGGAGCAACAGCAGACCCCTGCGCCACAGTGAGTCACTTCTACCAAGT 1380		
		1381	GTCCCAAGGCAACCGGCGCGGCTCTCTGTCCACATCGGTATCCCAGGCCGAGACACC 1440		
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		1501	TGCTAAAGATGAGGAAACTGAGGCTCAGAGGCTCAGAGGCTGAGTACCTGGCCCAAGGCCACACA 1560		
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		1561	GCCAGATCTTCCACTGAGTCACTGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAG 1620		
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		1621	GCAAGCACTTCGAGCTGCTGGCCCCCGAGAGGCTCACTGGAACTGCTTCTTAGCC 1680		
		1621	GCAAGCACTTCGAGCTGCTGGCCCCCGAGAGGCTCACTGGAACTGCTTCTTAGCC 1680		
		1681	CAGACCTTGGAGCTGAAGGCTCACCGCCAGTCCAGACAAAGTGAACAAAGATCAACAAAGA 1740		
		1681	CAGACCTTGGAGCTGAAGGCTCACCGCCAGTCCAGACAAAGTGAACAAAGATCAACAAAGA 1740		
		1741	CCTAACAGTTGCAAGATGAGCTGATAATTGTTGTTTATTATATATATATATATATATAT 1800		
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		1805	CCTAACAGTTGCAAGATGAGCTGATAATTGTTGTTTATTATATATATATATATATATAT 1805		
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RESULT 4
LOCUS AX140200 1722 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 6 from Patent WO0134796.
ACCESSION AX140200
VERSION AX140200.1 GI:14280539
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Toporoff, A., Biton, S., Savitzky, K. and Bernstein, J.
TITLE Chordin-like homologs
JOURNAL Patent: WO 0134796-A 6 17-MAY-2001;
COMPUGEN Ltd. (IL)
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 351 a 592 c 426 g 353 t
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Query Match 74.0%; Score 1344.4; DB 6; Length 1722;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

>y 424 TTGGGCTGGAGCCCTCTGGGACTAAATGGCACTGGTGGTTGGTGGAGCCCGAGACATGT 483
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>y 484 TCTGCTTTTCATGGGAAAGATATATCCCGCGGAGAGCTGGACCCCTACTTTGGAGC 543
>b 389 TCTGCTTTTCATGGGAAAGATATATCCCGCGGAGAGCTGGACCCCTACTTTGGAGC 448
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>y 604 ACCGCTTCACATGCTCCGCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
>b 509 ACCGCTTCACATGCTCCGCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
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>y 724 AGCAACAACGGGACCATGTATCAACAACGGGAGAGATCTTCAGTGCCCATGTGCTGCTGCTGCT 783
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>b 689 CCGCTGCTGCCAAACAGTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
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>y 904 AAGCTGCTCAAGATGAGGCAAGTGGAGCAATGGGATGAAGAGAGACATGTGGAGTGGCTGCTCC 963
>b 809 AGGCTGCTCAAGATGAGGCAAGTGGAGCAATGGGATGAAGAGAGACATGTGGAGTGGCTGCTCC 868
>y 964 ATGGGGTGGAGACATCTCTCAGGATCCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
>b 869 ATGGGGTGGAGACATCTCTCAGGATCCATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
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>y 1804 CATACCATCAAAA 1817
>b 1709 CATACCATCAAAA 1722

RESULT 5
AX119273 1792 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 5 from Patent WO0129084.
DEFINITION AX119273
ACCESSION AX119273
VERSION AX119273.1 GI:14036224
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Turner, C.A., Donoho, G., Nehls, M., Hilbun, E., Zambrowicz, B. and
Sands, A.T.
TITLE Human proteins and polynucleotides encoding the same
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JOURNAL Patent: WO 0125084-A 5 26-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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BASE COUNT 356 a 626 c 439 g 371 t
ORIGIN

Query Match 74.0%; Score 1344.4; DB 6; Length 1792;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCCCTCGGAGCTTAACTAGGACCTGCTGGTTTTCAGAGGCCAGAGATCT 483
DB 396 TGGAGCTCGGCTGCTCTGTTTCCCGCTGGACTCCCAAGCTCGAGCCGCGCCAGAGATCT 455
QY 484 TCTGCTTTTCCATGGGAGAGATCTCCCGCGGAGAGCTGCGACCCCTACTCTGGAGC 543
DB 456 TCTGCTTTTCCATGGGAGAGATCTCCCGCGGAGAGCTGCGACCCCTACTCTGGAGC 515
QY 544 CACAAGGCTGATGTAATCTGCTGGCTGTACTCTGCTCAGAGGGGCGCCATGTAGTGTGT 603
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QY 1804 CATAACCATCAAAA 1817
DB 1776 CATTACCTCAAAA 1789

RESULT 6
AX048199 1720 bp DNA linear PAT 15-DEC-2000
LOCUS Sequence 39 from Patent WO0070049.
DEFINITION AX048199
ACCESSION AX048199
VERSION AX048199.1 GI:11876989
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tang, Y.T., Yue, H., Lal, P., Burford, N., Bandman, O., Baughn, M.R.,
Azimzal, Y., Bu, D.A. and Patterson, C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 39 23-NOV-2000;
INCYTE Genomics, Inc. (US)
FEATURES
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BASE COUNT 357 a 592 c 425 g 346 t
ORIGIN

Query Match 73.9%; Score 1342.8; DB 6; Length 1720;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCCCTCGGAGCTTAACTAGGACCTGCTGGTTTTCAGAGGCCAGAGATCT 483
DB 321 TGGAGCTCGGCTGCTCTGTTTCCCGCTGGACTCCCAAGCTCGAGCCCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAAGAGATATCTCCCGGCGAGAGCTGGCACCCCTACTTTGAGC 543

[illegible]

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DB	821	AAGCCTTGCAAAATGAGCGAAGTACGATCCGATGAGAGGACATGTGTGCACTCGCTCC	880
QY	964	ATGGGTTGAGACATCCTCAGGATCCATGTTCCAGTGAATGCTGGGAGAAAGAGAGGCCGG	1023
DB	881	ATGGGTTGAGACATCCTCAGGATCCATGTTCCAGTGAATGCTGGGAGAAAGAGAGGCCGG	944
QY	1024	GCACCCCAGCCCCACTGSCCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTTACAG	1083
DB	941	GCACCCAGCCCCACTGSCCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTTACAG	1000
QY	1084	CCAGGGAGCGGACGACACAACTGTCCAGATCGTCTCTGAGGAGAAACATAGAAAGCT	1143
DB	1001	CCAGGGAGCGGACGACACAACTGTCCAGATCGTCTCTGAGGAGAAACATAGAAAGCT	1060
QY	1144	GTGTGATCGCGGGAAGACGTTATCTCCA CGGGAGAGTGTGGCA CCGGCGCTTCCGTGCT	1203
DB	1061	GTGTGATCGCGGGAAGACGTTATCTCCA CGGGAGAGTGTGGCA CCGGCGCTTCCGTGCT	1120
QY	1204	TCGCGCCCTTGCCCTGTCATCCTATGCACTCTGTAGGATGCGCGCAGGACTGCCAGGTG	1263
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QY	1264	TGACCTGTCCCA CCGAGTTACCCCTGCGGTCA CCCCAGAAAGTGGCTGGGAGTCTGCA	1323
DB	1181	TGACCTGTCCCA CCGAGTTACCCCTGCGGTCA CCCCAGAAAGTGGCTGGGAGTCTGCA	1240
QY	1324	AGATTTGCCCAGAGCAAAAGCAGACCCCTGGCCA CAGTGAGATCA GTTTCTACAGGTGTC	1383
DB	1241	AGATTTGCCCAGAGCAAAAGCAGACCCCTGGCCA CAGTGAGATCA GTTTCTACAGGTGTC	1300

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2b	1481	AGAATCTTCCACTTGACTTCAGATCAAGAAAGTCAGAGAGCAAGACTTCCAGAAAGAGCA	1540
2Y	1624	CAGCACTTCCGACTGCTGCTGGCCCGCCAGAGAGTCACTTGGAACTCTTCTAGCCAG	1683
2b	1541	CAGCACTTCCGACTGCTGCTGGCCCGCCAGAGAGTCACTTGGAACTCTTCTAGCCAG	1600
2Y	1684	ACCTTGAGCTGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT	1743
2b	1601	ACCTTGAGCTGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT	1660
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2b	1721	CATTACCTCAAAA	1734

RESULT 11

ACUS	AX140199	AX140199	1722 bp	DNA	linear	PAT 31-MAY-2001
DEFINITION	Sequence 5 from Patent WO0134796.					
ACCESSION	AX140199					
VERSION	AX140199.1	GI:4280538				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Toporik, A., Biton, S., Savitzky, K. and Bernstein, J.					
TITLE	Chordin-like homologs					
JOURNAL	Patent: WO 0134796-A 5 17-MAY-2001;					
FEATURES	CompuGen Ltd. (IL)					
source	Location/Qualifiers					
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BASE COUNT	351 a 594 c 425 g 352 t					
ORIGIN						
	Query Match	73.6%	Score 1338;	DB 6;	Length 1722;	
	Best Local Similarity	97.5%	Pred. NO. 0;			
	Matches 1359;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;	

QY	604	ACGCGCTCCACTGTCCGCTGCTCCACTGCGCCCGCCAGCTGTGACGGAGCCACAGCAATGCT	663
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QY	664	GTCCCAAGTGTGTGAACCTCACTCTCCCTCTGGAATCCGGGGCCCCACCAAGTCTGTC	723
DB	569	GTCCCAAGTGTGTGAACCTCACTCTCCCTCTGGAATCCGGGGCCCCACCAAGTCTGTC	628
QY	724	AGCAACAACGGGACCAATGTAACAACAAGGAGAGATCTTCAGTGGCCATGAGCTGTCCCT	783
DB	629	AGCAACAACGGGACCAATGTAACAACAAGGAGAGATCTTCAGTGGCCATGAGCTGTCCCT	688
QY	784	CCGCGCTGCGCCAAACAGTGTGCTCTGACGCTGCAACAGAGGSCAGATCTACTGCGGCC	843
DB	689	CCGCGCTGCGCCAAACAGTGTGCTCTGACGCTGCAACAGAGGSCAGATCTACTGCGGCC	748
QY	844	TCACACACTGCGCCGAACCAAGGCTGCGCAGCACCTCCGCTGCGCAGACTCTCTGCTGCC	903
DB	749	TCACACACTGCGCCGAACCAAGGCTGCGCAGCACCTCCGCTGCGCAGACTCTCTGCTGCC	808
QY	904	AAGCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCGATGCTGCTCC	963
DB	809	AAGCTTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCGATGCTGCTCC	868
QY	964	ATGCGGTGAGACATCTCCAGGATCCATGTTCCAGTGTGCTGCGGAGAGAGAGGCGCCGG	1023
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QY	1024	GCACCCCGCCCGCCAGCTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
DB	929	GCACCCCGCCCGCCAGCTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCATAC	988
QY	1084	CCAAGGAGCAGGCGAGCACTCTGTAAGATGCTCTGAGGAGAGAACTTGAAGAAGCT	1143
DB	989	CCAAGGAGCAGGCGAGCACTCTGTAAGATGCTCTGAGGAGAGAACTTGAAGAAGCT	1048
QY	1144	GTGTGATGCGCGGAGAGAGCTACTCCACCGGAGGAGTGTGCGACCGCGCTTCCTGCTGCT	1203
DB	1049	GTGTGATGCGCGGAGAGAGCTACTCCACCGGAGGAGTGTGCGACCGCGCTTCCTGCTGCT	1108
QY	1204	TCGCGCCCTTGTGCTGATCTCTATGCACTCTGTGAGGATGCGCGCCAGGAGCTGCCAGCTG	1263
DB	1109	TCGCGCCCTTGTGCTGATCTCTATGCACTCTGTGAGGATGCGCGCCAGGAGCTGCCAGCTG	1168
QY	1264	TGACCTTCCACCGAGTACCCCTGCGCTGCAACCGGAGGAGTGTGCGAGGAGTGTGCGA	1323
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QY	1384	CCAAGGACCGCGCGCGGCTCTCTGTCACACATCGGTATCCCAAGCCCGCAGACACCTGC	1443
DB	1289	CCAAGGACCGCGCGCGGCTCTCTGTCACACATCGGTATCCCAAGCCCGCAGACACCTGC	1348
QY	1444	GTGCTTTGCGCTGGAGACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG	1503
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QY	1564	AGAATCTTCCACTTGACTTCAGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGAGCA	1623
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Db	870	ATGGGATGAGACATCTCAGGATCCATGTTTCCAGTGTATGCTCGGAGAAAGAGGCGCG	929
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QY	1444	GTGCTTTGCCCTTGAAACACGAGGCTTGGAATCTGTGTGAGATCTACTCTCTGGAAGCTGG	1503
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QY	1564	AGAACTTTCCACTTGAACCTCAGATCAAGAAAGTCAAGGAAGACATCTCCAGAAAGGCA	1623
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LOCUS AX140204			
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ACCESSION AX140204			
VERSION AX140204.1			
KEYWORDS GI:14280543			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
linear PAT 31-MAY-2001			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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DEFINITION	AX119269	Version 1 GI:14036222				
ACCESSION	AX119269.1	GI:14036222				
VERSION						
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ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
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QY	484	TTGGCTTTTCATGGGAGAGATATCCCCCGCGAGAGCTGGACCCCTACTTTGGAGC	543			
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QY	544	CAAGAGGCTGATGTACTGCTGGCTGCTGATCTCTGCTCAGAGGGCGCCCATGTGAGTTGTT	603			
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QY	604	ACGGCTCCACTTCGCGCTGTCCACTGGCCCCAGCTGTGACGGAGCCACAGCAATGCT	663			
Db	215	ACGGCTCCACTTCGCGCTGTCCACTGGCCCCAGCTGTGACGGAGCCACAGCAATGCT	274			
QY	664	GTCCCAAGTGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCTGCC	723			
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QY	724	AGCACACGGGACCATGTATACCAACAGAGAGATCTTCAGTGCCCATGAGCTGTCCCTT	783			
Db	335	AGCACAAAGGACCATGTATACCAACAGAGAGATCTTCAGTGCCCATGAGCTGTCCCTT	394			
QY	784	CCGCTCCGCCACCAAGTGTGTCTCTGACAGCTGCACAGAGGGCCAGATCTACTGGGGC	843			
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QY	844	TCAAACTGCCCCGAAACCAAGCTGCCAGACCCCTCCGCTGCCAGATCTCTGTGGCC	903			
Db	455	TCAAACTGCCCCGAAACCAAGCTGCCAGACCCCTCCGCTGCCAGATCTCTGTGGCC	514			
QY	904	AGCCTGCAAAAGATAGGAGCAATGAGCAATCCGATGGAAGAGGACAGTGTGACGTCCCTC	963			
Db	515	ARGCCTGCAAAAGATAGGAGCAATGAGCAATCCGATGGAAGAGGACAGTGTGACGTCCCTC	574			
QY	964	ATGGGGTGAACATCTCTCAGGATCCATGTTCCAGTGTGGGAGAAAGAGAGGCCCGG	1023			
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QY	1024	GCAACCCAGCCCCCACTGGCTCTCAGCGCCCTCTCAGCTTCATCCCTGGCCACTTCAGAC	1083			
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DEFINITION	Sequence 1 from Patent WO0208277.								
ACCESSION	AX363199								
VERSION	AX363199.1	GI:18695336							
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	1								
AUTHORS	Alvarez,B.; Mcentire,J.K., Smith,R.C. and Su,E.W.								
TITLE	Nucleic acids, vectors, host cells, polypeptides, and uses thereof								
JOURNAL	Patent: WO 0208277-A 1 31-JAN-2002;								
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QY	484	TCGCTTTTTCATGGGAAGAGATACTCCCGCGAGAGCTGGACCCCTTCTTGGAGC	543						
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QY	1679	CCGACAGCCCTG	GAGCTG	GAAGTCC	AGGTC	CAAAAGT	GACCA	ATAACAAA	1738
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SOURCE									
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ORGANISM									
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
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1 Alvarez, J.K., Montire, J.K., Smith, R.C. and Su, E.W.									
Nucleic acids, vectors, host cells, polypeptides, and uses thereof									
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Db	122	CTTGCTTTT	CCATGG	CAAG	GAGAT	ACT	CCCC	CGG	181
QY	544	CACAGGCT	GTATG	TAT	CTG	CTG	CTG	TACT	603
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LOCUS
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AUTHORS
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JOURNAL
REMARK
COMMENT

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BC019399
BC019399.1 GI:18044155
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Strausberg, R.
Direct Submission
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
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QY	652 CACAGCAATGCTGCCCAAGTGTGTGAACTCACACTCCCTCTGCACTCCGGGCCCCAC	711	
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QY	712 CAAGTCTGCCAGCAACAAGGACCATGTATCCAAACAGGAGATCTTCAAGTGCCCATG	771	
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DEFINITION	Mus musculus chordin-related protein neuralin-2 mRNA, complete cds.		
ACCESSION	AF338222		
VERSION	AF338222.1 GI:13957540		
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Coffinier, C. C. and De Robertis, E. M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-JAN-2001) Biological Chemistry, UCLA - HMI, 675		
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y 592 ATGTGAGTTGTACGGCTCCTACTGTCCGCTGTCTCATGCCCCAGCTGTGAGGAGC 651
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y 832 TCTACTGGGCTCACAACCTGCCCGAACAGGCTGCCAGCACCCTCCCGCTGCCAG 891
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DEFINITION Sequence 19 from Patent WO9954353.
ACCESSION AX014311
VERSION AX014311.1 GI:10040665
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pillarsky,C.
Human nucleic acid sequences of normal uterus tissue
Patent: WO 9954353-A 19 28-Oct-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILLARSKY CHRISTIAN (DE)
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Matches 784; Conservative 0; Mismatches 16; Indels 59; Gaps 4;

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DEFINITION DRAFT SEQUENCE, 34 unordered pieces.
ACCESSION AP002010
VERSION AP002010.2 GI:8117625
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211452)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
Homo sapiens 211,452 genomic DNA of 11q14
Published Only in Database (2000)
2 (bases 1 to 211452)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.,
Direct Submission
Submitted (08-MAY-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7768935.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft11
Center clone name: RP11-880P3
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 189257 bases at least Q40
Consensus quality: 200319 bases at least Q30
Consensus quality: 205564 bases at least Q20
Insert size: 208152; sum-of-contigs
Quality coverage: 4.07X in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently consists of
34 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
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28122 42064 contig of 13943 bp in length
42165 45454 contig of 12380 bp in length
54645 54644 contig of 12290 bp in length
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67035 67034 contig of 100 bp
67035 78055 contig of 11031 bp in length
78066 78165 gap of 100 bp
78166 85965 contig of 7800 bp in length
85966 86085 gap of 100 bp
86086 94021 contig of 7956 bp in length
94022 94121 gap of 100 bp
94122 103137 contig of 9016 bp in length
103138 103237 gap of 100 bp
103238 110428 contig of 7191 bp in length
110429 110528 gap of 100 bp
110529 117261 contig of 6733 bp in length
117262 117361 gap of 100 bp
117362 124135 contig of 6774 bp in length
124136 124335 gap of 100 bp
124336 130539 contig of 6364 bp in length
130539 130690 gap of 100 bp
130690 136620 contig of 5921 bp in length
136620 136720 gap of 100 bp
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149361 149460 gap of 100 bp
149461 154813 contig of 5353 bp in length
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160815 160914 gap of 100 bp
160915 165830 contig of 4916 bp in length
165831 165930 gap of 100 bp
165931 171277 contig of 5347 bp in length
171278 171377 gap of 100 bp

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Sequence updated (26-May-2000).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 28121: gap of 100 bp
 42064: contig of 13943 bp in length
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 94121: gap of 100 bp
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SOURCE Mus sp.
ORGANISM Mus sp.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Toporik, A., Biton, S., Savitzky, K. and Bernstein, J.
TITLE Chordin-like homologs
JOURNAL Patent: WO 0134796-A 11 17-MAY-2001;
Compugen Ltd. (IL)
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Qy 1131 CATAGAGAGGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
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AX140205.1 GI:14280544
VERSION
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QY	653	ACAGCAATGCTGTCCAAAGTGTGTGGAACTCACACTCCCTCTGSACTCCGGGCCCCACC 712
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Qy 1301 GAAAGTGGCTGGGAAGTCTGCAAGATTTGGCCAGAGGA 1339

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AXI75120

LOCUS AXI75120 1864 bp DNA linear PAT 03-JUL-2001

DEFINITION Sequence 1 from Patent WO0142465.

ACCESSION AXI75120

VERSION AXI75120.1 GI:4598539

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1

AUTHORS Nakayama, N., Wen, D., Han, C. Y., He, C. and Yu, D.

TITLE Chordin-like molecules and uses thereof

JOURNAL Patent: WO 0142465-A 1 14-JUN-2001;

Amgen Inc. (US)

FEATURES

Location/Qualifiers

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BASE COUNT 527 a 422 c 375 g 540 t

ORIGIN

Query Match 11.6%; Score 211; DB 6; Length 1864;

Best Local Similarity 53.3%; Pred. No. 1.3e-45;

Matches 476; Conservative 0; Mismatches 405; Indels 12; Gaps 1;

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Db 408 TCATCTCTGTGCCCCCGCTGCCAGACTCTTACCAACAGTAAAGTGAACAG 467

Qy 713 AAAGTCTGCAGACACACGGGACATGTAACCAACGAGAGATCTTCAGTGGCCCATGA 772

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Db 528 GCTCTTTTCAAGAACCGGCAACCAATCATGTCGAGTCAGTGTAGCTGCTCGGAGGGAATGT 587

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THE UNIVERSITY OF CHICAGO

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DEFINITION Mus musculus ventroptin-alpha mRNA, complete cds.
ACCESSION AF321853
VERSION AF321853.1 GI:15341246
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1803)
AUTHORS Sakuta,H., Suzuki,R., Takahashi,H., Kato,A., Shintani,T., Iemura,S., Yamamoto,T.S., Ueno,N. and Noda,M.
TITLE Ventroptin: a BMP-4 antagonist expressed in a double-gradient pattern in the retina
JOURNAL Science 293 (5527), 111-115 (2001)
MEDLINE 21334726
PUBMED 11441185
REFERENCE 2 (bases 1 to 1803)
AUTHORS Sakuta,H. and Noda,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Molecular Neurobiology, National Institute for Basic Biology, 38 Nishigonaka, Myodai-icho, Okazaki, Aichi 444-8585, Japan
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Best local Similarity 53.5%; Pred. No. 2,8e-45;
Matches 470; Conservative 0; Mismatches 397; Indels 12; Gaps 1;
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DEFINITION Mus musculus cDNA clone IMAGE:6511005, partial cds.
ACCESSION BC050818
VERSION BC050818.1 GI:30046942
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3601)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheet,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., Woxley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huiyik,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Rodriguez,S., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Buetterfield,Y.S., Krzywinski,M.I., Skalek,U., Smaluk,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257

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12477932
 2 (bases 1 to 3601)
 Strausberg, R.
 Direct Submission
 Submitted (09-APR-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps@mail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 CDNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saedi, Jacqueline
 Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Nataaja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.
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 C 95 CTCAGACATATGCTGTTTCAGACAGAGATAGAGTGGGTGAGAAATGGCATCC 154
 Y 533 CTACTTGGAGCCACAGGCTGATGTTAGCTGCGCTGTACTCTCTCAGAGGGGCCCA 592
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 ACCESSION AF305714
 VERSION AF305714.1 GI:11037011
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 ORGANISM Mus musculus
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 Coffinier, C., Tran, U., Larrain, J. and De Robertis, E.M.
 Neuralin-1 is a novel Chordin-related molecule expressed in the
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 Coffinier, C.C. and De Robertis, E.M.
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Best Local Similarity 53.1%; Pred. No. 1e-44;
Matches 474; Conservative 0; Mismatches 407; Indels 12; Gaps 1;

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RESULT 39

BC002909

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

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BASE COUNT

ORIGIN

748 a 571 c 545 g 633 t

BC002909

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 15 Row: 0 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

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"

SULT 40
175126
CUS
FINITION
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YWORDS
URCE

751 ATCTCCACCAAGCCGACAGGCTGGAGTCTGTCCCGCTTCTCTGGGGCCAGAGTCACC 810
1060 GCTTCATCCTCGCCACTTCAGACCCCAAGGGAGCAGGCACAACTGTCAAAGATCGTCC 1119
811 GGGGAGCTCTTATGATTCCTCCAGCAGCATCAGGAACCATTTGTGCAATTGTCAATCAATA 870
1120 TGAAGAGAAACATTAAGAAAGCCTGTGTGCTGGGGAGACGTACTCCACGGGAGG 1179
871 ACAACACAAAGCATGGAATGTGTGTTTCCAAATGGAAGACCTATTCTCATGCGAGT 930
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1300 AGAAGTGGCTGGAGTGTCTGCAAGATTTGGCCAGAGGACAAAGCAGA 1348
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Search completed: January 31, 2004, 02:53:25
Job time : 6766 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

4 nucleic - nucleic search, using sw model

in on: January 30, 2004, 22:55:38 ; Search time 506 Seconds
(without alignments)
9693.437 Million cell updates/sec

file: US-09-890-456-8

Effect score: 1817

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Maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1817	100.0	1817	22	AAF84777
2	1772.2	97.5	1890	22	AAF84773
3	1417	78.0	1622	22	AAF84778
4	1344.4	74.0	1722	22	AAF84775
5	1344.4	74.0	1722	22	AA503538
6	1344.4	73.9	1720	22	AA503538
7	1342.8	73.9	1731	22	AA546065
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28	1274.4	70.1	1356	22	AA503536
29	1257	69.2	1497	23	AA584494
30	1256.4	69.1	1281	22	AAF84770
31	1222.8	67.3	1406	24	ABK12124
32	1222.8	67.3	1570	22	AA521152
33	1143.4	62.9	1290	22	AA503537
34	1139.2	62.7	1515	22	AAF84776
35	1121.4	61.7	1515	22	AAF84772
36	1038.4	57.1	1373	24	ABQ61159
37	1026.4	56.5	1517	24	ABK12125
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39	675.4	37.2	807	22	AA521151
40	543.6	29.9	622	23	AA575270
41	460	25.3	531	22	ABA60454
42	460	25.3	531	22	AAK08733
43	460	25.3	531	22	AAK34620
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ALIGNMENTS

RESULT 1

AAF84777
ID AAF84777 standard; DNA; 1817 BP.

AC AAF84777;

DT 09-JUL-2001 (first entry)

XX Nucleotide sequence of a human chordin-like homologue splice variant.

XX Splice variant; chordin like homologue; CLK; bone modelling; bone injury;
XX von-willebrand; factor type C repeat; VMFC repeat; bone formation;
XX reproductive disease; sexual differentiation; miscarriage; tumour;
XX sexual hormone; cardiovascular disorder; neuronal disease;
XX neurodegenerative disease; neuron development; ss.

OS Homo sapiens.

XX Location/Qualifiers

XX Key 414..1745

XX CDS /*tag= a

XX /product= "Chordin-like homologue splice variant"

XX

XX WO200134796-A1.

XX

XX 17-MAY-2001.

XX

XX 10-NOV-2000; 2000WO-IL00736.

XX

XX 10-NOV-1999; 99IL-0132846.

XX 28-DEC-1999; 99IL-0133767.

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661	QY	GCTGTCTCCAAAGTGTGTGGAACTCTCA	CACTCCCTCTGGA	CTCTCGGCGCCGCCACCAAGATGCT	720				
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1021	DB	CGGGACA	CCCGACGCCCCACTTGG	CTCTCAGCGGCCCTCTGAGCTTCA	TCCCTCGCGCATTC	1080			
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1141	DB	CTCTGTGTGCATGCGGGAGAACGTA	CTTCCCA	CGGGAGAGTGTGGCA	CCCGGCTCTCCGTG	1200			
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1201	DB	CTTTGCGGCCCTTGCCCTTG	CTGATCCTAT	GCACTGTGAGGATGGCGCCAGCACTGCCAGC	1260				
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Db	980	GCCTGCAAGATGAGCGAAGTGAAGATCGGATGAAGAGGACAGTGTGCAGTGCCTCCAT	1039
Qy	966	GGGTGAGACATCCTCAGGATCCATGTTCCAGTGAATGCTGGGAGAAAGAGAGCCGCGGC	1025
Db	1040	GGGTGAGACATCCTCAGGATCCATGTTCCAGTGAATGCTGGGAGAAAGAGAGCCGCGGC	1099
Qy	1026	ACCCAGCCGCCACTGGCTCAGCGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAGCC	1085
Db	1100	ACCCAGCCGCCACTGGCTCAGCGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAGCC	1159
Qy	1086	AGGAGGAGGAGGACGACACACTGTCAGATGCTCCTGAGGAGAAACATNAGAAAGCTGT	1145
Db	1160	AGGAGGAGGAGGACGACACACTGTCAGATGCTCCTGAGGAGAAACATNAGAAAGCTGT	1219
Qy	1146	GTGCATGGCGGGAAGACGTATCTCCACGCGGAGGTGTGCACCCGGGCTTCGGTGCCTTC	1205
Db	1220	GTGCATGGCGGGAAGACGTATCTCCACGCGGAGGTGTGCACCCGGGCTTCGGTGCCTTC	1279
Qy	1206	GGCCCTTGGCCCTGCATCTCTATGACACCTGTGAGGATGGCCGCGAGGACTCCAGAGGTGT	1265
Db	1280	GGCCCTTGGCCCTGCATCTCTATGACACCTGTGAGGATGGCCGCGAGGACTCCAGAGGTGT	1339
Qy	1266	ACCTGTCCACCGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAAGTCTCTCAAG	1325
Db	1340	ACCTGTCCACCGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAAGTCTCTCAAG	1399
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Qy	1446	CGCTTGGCCCTGGAACACGAGGSCCTCGGACCTTGGTGGAGATCTACCTCTGGAAGCTGGTA	1505
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Qy	1506	AAAGTGAAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAG	1565
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XX	AAF84778;		
AC	AAF84778;		
XX	09-JUL-2001	(first entry)	
DT			

XX	DE	Nucleotide sequence of a human chordin-like homologue splice variant.
XX	XX	
XX	XX	Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
XX	XX	von-Willebrand factor type C repeat; VWFC repeat; bone formation;
XX	XX	reproductive disease; sexual differentiation; miscarriage; tumour;
XX	XX	sexual hormone; cardiovascular disorder; neuronal disease;
XX	XX	neurodegenerative disease; neuron development; ss.
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PD	XX	17-MAY-2001.
XX	XX	
PF	XX	10-NOV-2000; 200WO-IL00736.
XX	XX	
PR	XX	10-NOV-1999; 99IL-0132846.
PR	XX	28-DEC-1999; 99IL-0133767.
XX	XX	(COMP-) COMPUGEN LTD.
PA	XX	Toporolk A, Biton S, Savitzky K, Bernstein J;
PI	XX	WPI: 2001-308783/32.
XX	XX	P-PSDB; AN568081.
DR	XX	Nucleic acids encoding splice variants of a chordin like homolog,
XX	XX	useful in the treatment of bone injuries, diseases involved with the
PI	XX	female reproductive tract, diseases involving sexual hormone
PT	XX	abnormalities and cardiovascular disorders -
XX	XX	
PS	XX	Claim 1; Page 183; 203pp; English.
XX	XX	
CC	XX	The present sequence encodes a splice variant of a chordin like
CC	XX	homologus (CLH). The protein is a homologue to the known chordin within
CC	XX	the von-Willebrand factor type C (VWFC) domain repeat, which is found 2-4
CC	XX	times in these multi-domain proteins. The present protein contains 2
CC	XX	VWFC repeats. CLH proteins and polynucleotides can be used for the
CC	XX	treatment of diseases which can be ameliorated, cured or prevented by
CC	XX	raising the level of a CLH. The nucleic acids, expression vectors
CC	XX	and proteins and antibodies are useful in the treatment of a disease selected
CC	XX	from diseases manifested in non-normal bone formation and non-normal bone
CC	XX	modelling, bone injuries, diseases involved with the female reproductive
CC	XX	tract, diseases of disorders involved with abnormal sexual
CC	XX	differentiation, recurrent miscarriages, tumours of the uterus, breast
CC	XX	or prostate, diseases involving sexual hormone abnormalities,
CC	XX	cardiovascular disorders, neuronal diseases of the CNS (central nervous
CC	XX	system), or neurodegenerative diseases and diseases involving non-normal
CC	XX	developments of neurons.
XX	XX	
SQ	XX	Sequence 1622 BP; 411 A; 468 C; 417 G; 326 T; 0 other;
Query Match		78.0%; Score 1417; DB 22; Length 1622;
Best Local Similarity		89.3%; Pred. No. 0;
Matches 1622;		Conservative 0; Mismatches 0; Indels 195; Gaps 1;
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Db	61	GAGACTGTGTGTCATGCTGCTGGTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy	121	TTACCCCTCTGGGCTCATTTGCTCTAATCATATAATTAATTAACGCTGATACCATGATATA 180
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1139 ----- 1138
1321 GCAAGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAATCAGTTCTACAGGT 1380
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1801 TTGCATAACCATCAAAA 1817
1606 TTGCATAACCATCAAAA 1622

RESULT 4
AAF84775
ID AAF84775 standard; DNA; 1722 BP.
XX AC AAF84775;
XX DT 09-JUL-2001 (first entry)
XX DE Nucleotide sequence of a human chordin-like homologue splice variant.
XX KW Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
XX KW von-Willebrand factor type C repeat; VWFC repeat; bone formation;
XX KW reproductive disease; sexual differentiation; miscarriage; tumour;
XX KW sexual hormone; cardiovascular disorder; neuronal disease;
XX KW neurodegenerative disease; neuron development; ss.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
FH CDS 1..1650
FT /*tag= a
FT /product= "chordin-like homologue splice variant"
XX PN WC200134796-A1.
XX XX PD 17-MAY-2001.
XX XX PF 10-NOV-2000; 2000WO-IL00736.
XX XX PR 10-NOV-1999; 99IL-0132846.
XX XX PR 28-DEC-1999; 99IL-0133767.
XX XX

181 ATCTGTACAGCATTTCACTGCTGATTCCCTAACTGCGCCTGTGAGATTAAGGCTTAAAGGCT 240
181 ATCTGTACAGCATTTCACTGCTGATTCCCTAACTGCGCCTGTGAGATTAAGGCTTAAAGGCT 240
241 CAGAGACAGTGGCATGTGCCCATGTTCGACATGTAAGTGTGTGTAAGCCGAGATTCAAAC 300
241 CAGAGACAGTGGCATGTGCCCATGTTCGACATGTAAGTGTGTGTAAGCCGAGATTCAAAC 300
301 TCAGACCTTCTGGCCCTTGCCTAGAGAGACATGCCAGATGTGTCTAGCAGATTCTCTTTT 360
301 TCAGACCTTCTGGCCCTTGCCTAGAGAGACATGCCAGATGTGTCTAGCAGATTCTCTTTT 360
361 GCCTGAGTGGCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAGAAATGAGACAGGG 420
361 GCCTGAGTGGCCAGATGACATCTCTTTTAGAGCTAGAAAAGAGGAGAAATGAGACAGGG 420
421 TCTTTGGGCTGGAGCTCTGGGACTTAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 TCTTTGGGCTGGAGCTCTGGGACTTAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 TGTTCCTGCTTTTCATGGAAGAGATATCCTCCCGGCGAGAGCTGGCACCCCTACTTGG 540
481 TGTTCCTGCTTTTCATGGAAGAGATATCCTCCCGGCGAGAGCTGGCACCCCTACTTGG 540
541 AGCCACAAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 AGCCACAAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
601 GTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 GTTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
661 GCTGTCCCAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCCACCAAGTCC 720
661 GCTGTCCCAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCCACCAAGTCC 720
721 GCCAGACAAACCGGACCATGTACCAACAGAGAGATCTTCAAGTGCCTCATGAGCTGTTC 780
721 GCCAGACAAACCGGACCATGTACCAACAGAGAGATCTTCAAGTGCCTCATGAGCTGTTC 780
781 CCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
781 CCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
841 GCCTCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
841 GCCTCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
901 GCCAAGCTGCAAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
901 GCCAAGCTGCAAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
961 TCATCGGCTGAGATCATCTCAGGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
961 TCATCGGCTGAGATCATCTCAGGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
1021 CGGCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGAC 1080
1021 CGGCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGAC 1080
1081 GACCAAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1140
1081 GACCAAGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1140
1141 CCTGTGTGATGCTGCGGAGAGCTGCTCCCAAGGAGGAGTGTGCGCCGCTTCCGCTG 1200
1139 ----- 1138
1201 CTTTGGGCCCCCTTGGCCCTGGCATCTATGACACTGTGAGGATGGCGCGCAGAGCTGCCAGC 1260
1139 ----- 1138

(COMP-) COMPUGEN LTD.
Toporok A, Biton S, Savitzky K, Bernstein J;
WPI; 2001-308783/32.
P-PSDB; AAB68078.
Nucleic acids encoding splice variants of a chordin like homolog, the useful in the treatment of bone injuries, diseases involved with the female reproductive tract, diseases involving sexual hormone abnormalities and cardiovascular disorders -
Claim 1; Page 181; 203pp; English.
The present sequence encodes a splice variant of a chordin like homologue (CLH). The protein is a homologue to the known chordin within times in these multi-domain proteins. The present protein contains 3 WMFC repeats. CLH proteins and polynucleotides can be used for the treatment of diseases which can be ameliorated, cured or prevented by raising the level of a CLH. The nucleic acids, expression vectors, proteins and antibodies are useful in the treatment of a disease selected from diseases manifested in non-normal bone formation and non-normal bone modelling, bone injuries, diseases involved with the female reproductive tract, diseases of disorders involved with abnormal sexual differentiation, recurrent miscarriages, tumors of the uterus, breast or prostate, diseases involving sexual hormone abnormalities, cardiovascular disorders, neuronal diseases of the CNS (central nervous system), or neurodegenerative diseases and diseases involving non-normal developments of neurons.
Sequence 1722 BP; 351 A; 592 C; 426 G; 353 T; 0 other;

Query Match 74.0%; Score 1344.4; DB 22; Length 1722;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
424 TTGGGCTGGAGCTCTCTGGGCTAAACATGCACTGTGCTGCTTCCAGGCGCCAGACATGT 483
329 TGGGACTCGCGTCTCTGTGCTCCCTGCTGACTCCACGCTCGAGCGCCGACAGATGT 388
484 TCTGCTTTCCATGGGAAGAGATCTCTCCCGGAGAGCTGTCACCCCTACTTGGAGC 543
389 TCTGCTTTCCATGGGAAGAGATCTCTCCCGGAGAGCTGTCACCCCTACTTGGAGC 448
544 CACAAGGCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGCGCCCATGTGATGT 603
449 CACAAGGCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGCGCCCATGTGATGT 508
604 ACCGCTTCACTGTCGCTGTCCTCACTGCCCCCAGCGCTGTGACGAGCCACAGCAATGCT 663
509 ACCGCTTCACTGTCGCTGTCCTCACTGCCCCCAGCGCTGTGACGAGCCACAGCAATGCT 568
664 GTCCCAAGTGTGGAACTCACTACCTCTGGAATCCCGGCGCCACCAAGTCTGCG 723
569 GTCCCAAGTGTGGAACTCACTACCTCTGGAATCCCGGCGCCACCAAGTCTGCG 628
724 AGCAACAGGAGCATGTATCCAAACAGGAGAGATCTTCAAGTCCCAAGAGCTTCCCT 783
629 AGCAACAGGAGCATGTATCCAAACAGGAGAGATCTTCAAGTCCCAAGAGCTTCCCT 688
784 CCGGCTTCCCAACAGTGTCTCTCTGCTGAGCTGCAAGAGGCGCCAGATCTACTGCGGC 843
689 CCGGCTTCCCAACAGTGTCTCTCTGCTGAGCTGCAAGAGGCGCCAGATCTACTGCGGC 748
844 TCACAACCTGCGCCGAGAGCTGCTCCAGAGAGCTGCTCCGCTGCGAGCTCTCTGCTGC 903
749 TCACAACCTGCGCCGAGAGCTGCTCCAGAGAGCTGCTCCGCTGCGAGCTCTCTGCTGC 808
904 AAGCTGCAAGATGAGGAGAGTGTGAGAGATCGATGAGAGAGAGTGTGAGTGTGCTCC 963
809 AGGCTGCAAGAGTGGAGAGTGTGAGAGATCGATGAGAGAGAGTGTGAGTGTGCTCC 868

964 ATGGGCTGAGACATCTTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 1023
869 ATGGGCTGAGACATCTTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 928
1024 GCACCCGAGCCGCTGAGCTGCTGAGCTTCACTCCCTGAGCTTCACTCCCTGAGCTTCACT 1083
929 GCACCCGAGCCGCTGAGCTGCTGAGCTTCACTCCCTGAGCTTCACTCCCTGAGCTTCACT 988
1084 CCAAGGAG 1143
989 CCAAGGAG 1048
1144 GTGTGATGCTGCGGAG 1203
1049 GTGTGATGCTGCGGAG 1108
1204 TCGGCGCTTTCGCTGATCTATGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1263
1109 TCGGCGCTTTCGCTGATCTATGACACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1168
1264 TGACCTGTCCACCGAGTACCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1323
1169 TGACCTGTCCACCGAGTACCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1228
1324 AGATTGCTCCAG 1383
1229 AGATTGCTCCAG 1288
1384 CCAAGGAG 1443
1289 CCAAGGAG 1348
1444 GTGCTTTCGCTGAG 1503
1349 GTGCTTTCGCTGAG 1408
1504 TAAAGATGAG 1563
1409 TAAAGATGAG 1468
1564 AGAATCTTCACCTGAG 1623
1469 AGAATCTTCACCTGAG 1528
1624 CAGCACTTCGAG 1683
1529 CAGCACTTCGAG 1588
1684 ACCCTGAG 1743
1589 ACCCTGAG 1648
1744 AACAGTTGAG 1803
1649 AACAGTTGAG 1708
1804 CATACCATCAAAA 1817
1709 CATACCATCAAAA 1722
RESULT 5
AAS03538
ID AAS03538 standard; cDNA; 1792 BP.
XX AAS03538;
AC AAS03538;
DT 29-AUG-2001 (first entry)
XX cDNA encoding Novel Human Protein, NHP #1, ORF and flanking sequences.
DE Human; Novel Human Protein; NHP; diagnostic; drug screening; cancer;
KW clinical trial monitoring; physiological disorder; behavioural disorder;

infectious disease; gene therapy; ss.

Homo sapiens.

Key Location/Qualifiers
3'UTR 1..360 /tag= a
CDS 361..1717 /tag= b
5'UTR 1718..1792 /tag= c

WO200129084-A2.

26-APR-2001.

18-OCT-2000; 2000WO-US28803.

18-OCT-1999; 99US-0160106.

29-OCT-1999; 99US-0162547.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Donoho G, Nehls M, Hilbun E, Zambrowicz B, Sands AT;
WPI; 2001-290898/30.
P-PSDB; AAU02749.

Nucleic acids encoding novel human proteins (NHP), useful for treating physiological or behavioural disorders, cancers and infectious diseases

Disclosure; Page 61; 63pp; English.

The sequence represents the coding sequence of a novel human protein, NHP #1, including open reading frame (ORF) and flanking sequences, are isolated from a human adrenal gland cDNA library. NHP nucleotides are useful for drug screening and clinical trial monitoring, and for the diagnosis and treatment of physiological or behavioural disorders, cancer and infectious disease. Nucleotide constructs encoding functional NHPs, mutant NHPs, as well as antisense and ribozyme molecules can also be used in gene therapy for the modulation of NHP expression. NHP polypeptides may be used to produce agonists, antagonists and antibodies for the regulation of NHP expression in the treatment and/or diagnosis of disease.

Sequence 1792 BP; 356 A; 626 C; 439 G; 371 T; 0 other;

Query Match 74.08; Score 1344.4; DB 22; Length 1792;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

424 TTGGGCTGGAGCCTCTGGGACTTAACATGGACATGGTGGTGGTGGCCAGACATGT 483
b 396 TGGGACTCGCGCTGCTGTGGTTCCTCCCTGGACTCCACGCTCGAGCCGCGCAGACATGT 455
y 484 TCTGCTCTTTCATGGCAAGAGATATCTCCCGGCGGAGAGCTGGCACCCCTACTTTGGAGC 543
b 456 TCTGCTCTTTCATGGCAAGAGATATCTCCCGGCGGAGAGCTGGCACCCCTACTTTGGAGC 515
y 544 CACAGGCTGATCTACTGCTGGCTGTACTGCTGTACTGCTGTACTGCTGTACTGCTGTACTGCTGT 603
b 516 CACAGGCTGATGATGCTGCTGCTGTACTGCTGTACTGCTGTACTGCTGTACTGCTGTACTGCTGT 575
y 604 ACCGCTTCACTGTCCGCTGTCTCACTGCGCCCTGAGCTGTGACGAGAGCAAGCAATGCT 663
b 576 ACCGCTTCACTGTCCGCTGTCTCACTGCGCCCTGAGCTGTGACGAGAGCAAGCAATGCT 635
y 664 GTCCCAAGTGTGTGAACCTCACACTCCCTGTGAGCTCCGGGCCCCCAGCAAAAGTCTGCCC 723
b 636 GTCCCAAGTGTGTGAACCTCACACTCCCTGTGAGCTCCGGGCCCCCAGCAAAAGTCTGCCC 695

QY 724 AGCA CAA CGG GGA CCA TGT ACC AA CAG GAG A GAT TTT CAG TGC CCA TGA GCT GTT C C C C T 783
DB 696 AGCA CAA CGG GGA CCA TGT ACC AA CAG GAG A GAT TTT CAG TGC CCA TGA GCT GTT C C C C T 755
QY 784 CCG C C T G C C C A A C A G T G T G T C C T C T G C A G C T G C A C A G A G G G C C A G A T A C T A C T C G G G C C 843
DB 756 CCG C C T G C C C A A C A G T G T G T C C T C T G C A G C T G C A C A G A G G G C C A G A T A C T A C T C G G G C C 815
QY 844 T C A C A C C T G C C C G A A C A G G C T G C C C A G C A C C C C T C C C G C T G C C A G A C T C C T G C T G C C 903
DB 816 T C A C A C C T G C C C G A A C A G G C T G C C C A G C A C C C C T C C C G C T G C C A G A C T C C T G C T G C C 875
QY 904 A G C C T G C A A A G A T G A G G C A A G T G A G C A A T G G A T G A A G A G A C A G T G T G C A G T C G C T C C 963
DB 876 A A G C C T G C A A A G A T G A G G C A A G T G A G C A A T G G A T G A A G A G A C A G T G T G C A G T C G C T C C 935
QY 964 A T G G G T G A G A C A T C C T C A G G A T C C A T G T T C C A G T G A T G C T G G G A A A A G A G A G C C C G G 1023
DB 936 A T G G G T G A G A C A T C C T C A G A T C C A T G T T C C A G T G A T G C T G G G A A A A G A G A G C C C G G 995
QY 1024 G C A C C C A G C C C C A C T G G G C C T C A G G C C C C T C T G A G C T T C A T C C C T G C C C A C T T C A G A C 1083
DB 996 G C A C C C A G C C C C A C T G G G C C T C A G G C C C C T C T G A G C T T C A T C C C T G C C C A C T T C A G A C 1055
QY 1084 C A A G G A G C A G G C A G C A C A C T G T C A G A T G C T C T G A A G A G A A A C A T A A A A G C C T 1143
DB 1056 C C A A G G A G C A G G C A G C A C A C T G T C A A G A T C G T C T G A A G G A G A A C A T A A A A G C C T 1115
QY 1144 G T G T G C A T G G C G G A A G A C G T A C T C C A C G G G A G G T G T G G C A C C G G C C T T C C G T G C C T 1203
DB 1116 G T G T G C A T G G C G G A A G A C G T A C T C C A C G G G A G G T G T G G C A C C G G C C T T C C G T G C C T 1175
QY 1204 T C G G C C C T T G C C T G C A T C C T A T G C A C C T G T G A G A T G C C C C A G A C T G C C A G A G G T G 1263
DB 1176 T C G G C C C T T G C C T G C A T C C T A T G C A C C T G T G A G A T G C C C C A G A G G T G C C A G C G T G 1235
QY 1264 T G A C T G T C C C A C G A G T A C C C T G C C T C A C C C G A A G T G C T G G G A G T G C T G C A 1323
DB 1236 T G A C T G T C C C A C G A G T A C C C T G C C T C A C C C G A A A G T G G C T G G A A G T G C T G C A 1295
QY 1324 A G A T T T G C C A G A G A C A A A G A G A C C C T G G C C A C A G T A G A T C A G T T T C A C A G G T G T C 1383
DB 1296 A G A T T T G C C A G A G A C A A A G A G A C C C T G G C C A C A G T A G A T C A G T T T C A C A G G T G T C 1355
QY 1384 C C A A G C A C C G G G C G G G T C C T C G T C C A C A C A T C G G T A T C C C A G C C C A G C A C A C C T G C 1443
DB 1356 C C A A G C A C C G G G C G G G T C C T C G T C C A C A C A T C G G T A T C C C A G C C C A G C A C A C C T G C 1415
QY 1444 G T C G C T T T G C C C T G B A C A C A G A G G C C T G G A C T T G T G G A G A T C T A C C T C T G B A G C T G G 1503
DB 1416 G T C G C T T T G C C C T G B A C A C A G A G G C C T G G A C T T G T G G A G A T C T A C C T C T G B A G C T G G 1475
QY 1504 T A A A G A T G A G A A A C T G A G G C T C A G A G A G T G A A G T A C C T G G C C C A G G C C A C A C A G C C 1563
DB 1476 T A A A G A T G A G A A A C T G A G G C T C A G A G A G T G A A G T A C C T G G C C C A G G C C A C A C A G C C 1535
QY 1564 A G A A T C T T C C A C T T T G A C T C A G A T C A A G A A A T C A G G A A G C A A G A C T T C C A G A A A G A G G C A 1623
DB 1536 A G A A T C T T C C A C T T T G A C T C A G A T C A A G A A A T C A G G A A G C A A G A C T T C C A G A A A G A G G C A 1595
QY 1624 C A G C A C T C C G A C T G C T G C G C C C C C C A C A G A G T C A C T G G A A G C T C T C T C A G C C C A G 1683
DB 1596 C A G C A C T C C G A C T G C T G C G C C C C C C A C A G A G T C A C T G G A A G C T C T C T C A G C C C A G 1655
QY 1684 A C C T G G A G C T G A A G G T C A G G C C A G T C C A C A A A G T G A C C A A G A C A T A C A A A G C C T 1743
DB 1656 A C C T G G A G C T G A A G G T C A G G C C A G T C C A C A A A G T G A C C A A G A C A T A C A A A G C C T 1715
QY 1744 A A C A G T T G C A G A T A G C T G T A T A A T T G T T A T T A T A T A T T A T A T A T A A A A A G A A G T T G 1803
DB 1716 A A C A G T T G C A G A T A G C T G T A T A A T T G T T A T A T A T A T A T A T A T A T A A A A A G A A G T T G 1775
QY 1804 C A T A A C C A T C A A A A 1817

CC associated disorders, as targets in microarray, to generate hybridization
CC probes and to detect differences in gene sequences among normal, carrier
CC or affected individuals. Antibodies may also be used in diagnosing
CC disorders, in monitoring patients being treated with EXCS agonists,
CC antagonists or inhibitors. Sequences AAC84293-84318 represent nucleic
CC acid molecules encoding the EXCS of the invention.

XX
SQ Sequence 1720 BP; 357 A; 592 C; 425 G; 346 T; 0 other;

Query Match 73.9%; Score 1342.8; DB 22; Length 1720;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGGCTGGAGCTCTCGGAGCTAAACATGCACTGTGGTTCCTCCAGCGCCAGACATGT 483
Db 321 TGGGACTCGCGCTGTCTGGTTCCTCCAGCTCCGAGCGCCAGACATGT 380
Qy 484 TCTGCTTTTCCATGGGAGAGATCTCCCGGGGAGAGCTGCACCCCTACTCTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAGAGATCTCCCGGGGAGAGCTGCACCCCTACTCTGGAGC 440
Qy 544 CACAAGGCTGATGTACTGTCTGCTGTACTCTCAGAGGGGCCCATGTAGTTGT 603
Db 441 CACAAGGCTGATGTACTGTCTGCTGTACTCTCAGAGGGGCCCATGTAGTTGT 500
Qy 604 ACCGCTCCCACTGTCCGCTGTCCCACTGCCCGCCAGCCTGTGACGGAGCCACAGCAATGT 663
Db 501 ACCGCTCCCACTGTCCGCTGTCCCACTGCCCGCCAGCCTGTGACGGAGCCACAGCAATGT 560
Qy 664 GTCCCAAGTGTGGAACTCCTACACTCCTCTGACTCCGGGCCCCCAACAAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCCTACACTCCTCTGACTCCGGGCCCCCAACAAAGTCTCTGCC 620
Qy 724 AGCACAAGGAGCATGTACCAACAGGAGAGATCTTCAGTGCCTCAGTCTCTCCCT 783
Db 621 AGCACAAGGAGCATGTACCAACAGGAGAGATCTTCAGTGCCTCAGTCTCTCCCT 680
Qy 784 CCSCCTGCCCAACAGTGTCTCTGAGCTGCAACAGAGGCGCAGATCTATCTGCGGCC 843
Db 681 CCSCCTGCCCAACAGTGTCTCTGAGCTGCAACAGAGGCGCAGATCTATCTGCGGCC 740
Qy 844 TCACAACCTGCCCGGAAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGTCTGCC 903
Db 741 TCACAACCTGCCCGGAAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGTCTGCC 800
Qy 904 AAGCTGCAAGATGAGGCAAGTGCAGATCGATCGATCGATCGATCGATCGATCGATCGAT 963
Db 801 AAGCTGCAAGATGAGGCAAGTGCAGATCGATCGATCGATCGATCGATCGATCGATCGAT 860
Qy 964 ATGGGGTGAGACATCTCTAGGATCCATGTTCCAGTGTCTGAGTGTCTGAGTGTCTGAGT 1023
Db 861 ATGGGGTGAGACATCTCTAGGATCCATGTTCCAGTGTCTGAGTGTCTGAGTGTCTGAGT 920
Qy 1024 GCACCCGAGCCGCCCACTGGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 1083
Db 921 GCACCCGAGCCGCCCACTGGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCT 980
Qy 1084 CCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143
Db 981 CCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1040
Qy 1144 GTGTGATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
Db 1041 GTGTGATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
Qy 1204 TCGGCCCTTGGCCCTGATCTCTATGACATCTGTGAGATGGCCCGCAGGAGCTGCCAGCGTG 1263
Db 1101 TCGGCCCTTGGCCCTGATCTCTATGACATCTGTGAGATGGCCCGCAGGAGCTGCCAGCGTG 1160
Qy 1264 TGACCTGTCCCAACAGGAGTACCCCTTCCCTCACCCTCCGAGAAAGTGGCTGGGAAAGTGTGCA 1323
Db 1161 TGACCTGTCCCAACAGGAGTACCCCTTCCCTCACCCTCCGAGAAAGTGGCTGGGAAAGTGTGCA 1220

Db 1776 CATTACCTGAAA 1789
RESULT 6
AAC84305
ID AAC84305 standard; cDNA; 1720 BP.
XX AAC84305;
XX AC AAC84305;
DT 19-MAR-2001 (first entry)
XX Human EXCS encoding cDNA (clone ID 2267403CB1).
XX Extracellular signaling molecule; EXCS: anti-inflammatory; human;
XX immunosuppressive; cytosolic; neuroprotective; Gastrointestinal;
XX virulence; antibacterial; anti-HIV; human immunodeficiency virus;
XX antifertility; cerebroprotective; neurotropic; antitumor; antifungal;
XX anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
XX keratolytic; protozoicide; gene therapy; ss.
XX Homo sapiens.
XX W0200070049-A2.
XX 23-NOV-2000.
XX 19-MAY-2000; 2000WO-US13975.
XX 19-MAY-1999; 99US-0134949.
XX 15-JUL-1999; 99US-0144270.
XX 30-JUL-1999; 99US-0146700.
XX 04-OCT-1999; 99US-0157508.
XX (INCY-) INCYTE GENOMICS INC.
XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX Azimzai Y, Lu DAM, Patterson C;
XX WPI: 2001-025021/03.
XX P-PSDB; AAB48069.
XX New human extracellular signaling nucleic acids and polypeptides useful
XX for diagnosing, treating and preventing infections and
XX gastrointestinal, neurological, reproductive, and
XX autoimmune/inflammatory disorders -
XX Claim 4; Page 105-106; 114pp; English.
XX The invention provides human extracellular signaling molecules (EXCS)
XX and polynucleotides which identify and encode EXCS. EXCS can be
XX expressed by standard recombinant methodology. The amino acid and nucleic
XX acid sequences of EXCS are useful for diagnosing, treating and
XX preventing infections and gastrointestinal (peptic ulcer, dysphagia,
XX pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
XX disease, stroke), reproductive (infertility, ovulatory defects, acquired
XX immunodeficiency syndrome (AIDS), Addison's disease), and cell
XX endometrial disorders including cancers (of the breast, adrenal gland,
XX bone). They may also be used to treat fatal familial insomnia,
XX nutritional and metabolic diseases of the nervous system, myopathies,
XX mental disorders (anxiety, schizophrenia, mood), as well as infections
XX caused by parasites (malaria, leishmania, trypanosoma), viral
XX (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
XX staphylococcus, bacillus), and fungal (aspergillus, blastomycosis,
XX dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
XX agonists, pharmaceutical compositions, and antibodies may also be used
XX for treating or preventing disorders associated with increased or
XX decreased expression or activity of EXCS. EXCS polynucleotides may also
XX be used to detect and quantify gene expression in biopsied tissues in
XX which expression of EXCS may be correlated with the disease, to determine
XX presence or excess expression of EXCS, to monitor regulation of EXCS
XX levels during therapeutic intervention, to detect the presence of

1324 AGATTTGGCCAGAGGACAAAGACAGACCCCTGGCCACAGTCAGATCGATCTTACCAGGTGTC 1383
1221 AGATTTGGCCAGAGGACAAAGACAGACCCCTGGCCACAGTCAGATCGATCTTACCAGGTGTC 1280
1384 CCAAGGCAACGGGCGGGTCTCGTCCACATCGGTATCCCGAGCCACAGCAACCTGC 1443
1281 CCAAGGCAACGGGCGGGTCTCGTCCACATCGGTATCCCGAGCCACAGCAACCTGC 1340
1444 GTCCGCTTTGCCCTGGAAACAGAGGCTCTGGATCTTGGTGGAGATCTACTCTCTGGAGCTGG 1503
1341 GTCCGCTTTGCCCTGGAAACAGAGGCTCTGGATCTTGGTGGAGATCTACTCTCTGGAGCTGG 1400
1504 TAAAGATGAGGAACTAGGCTCTAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
1401 TAAAGATGAGGAACTAGGCTCTAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1623
1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1520
1624 CAGCACTTCGCACTGCTCGTGGCCGCCAGAAAGTCTACTGGAAAGTCTTCTTACGCCAG 1683
1521 CAGCACTTCGCACTGCTCGTGGCCGCCAGAAAGTCTACTGGAAAGTCTTCTTACGCCAG 1580
1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAAAGTGAACACATACAAAGACCT 1743
1581 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAAAGTGAACACATACAAAGACCT 1640
1744 AACAGTTGAGATATGAGCTGATATATTTGTTTATTATATATTAATAAAGAGTTG 1803
1641 AACAGTTGAGATATGAGCTGATATATTTGTTTATTATATTAATAAAGAGTTG 1700
1804 CATTAACCATCAAAA 1817
1701 CATTAACCATCAAAA 1714

RESULT 7
AS46065
D AAS46065 standard; cDNA; 1731 BP.
X C AAS46065;
X T 18-DEC-2001 (first entry)
T Human DNA encoding PRO polypeptide sequence #141.
E PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
W dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
W blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
W adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
W PCR primer.
X Homo sapiens.
S WO200168848-A2.
N 20-SEP-2001.
D 28-FEB-2001; 2001WO-US06520.
F 01-MAR-2000; 2000WO-US05601.
X 02-MAR-2000; 2000WO-US05841.
R 03-MAR-2000; 2000US-187202P.
R 06-MAR-2000; 2000US-186968P.
R 14-MAR-2000; 2000US-189320P.
R 14-MAR-2000; 2000US-189328P.
R 15-MAR-2000; 2000WO-US06884.
R 21-MAR-2000; 2000US-190828P.
R 21-MAR-2000; 2000US-191007P.
R 21-MAR-2000; 2000US-191048P.
R 21-MAR-2000; 2000US-191314P.
R 28-MAR-2000; 2000US-192655P.

29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX (GBTH). GENENTECH INC.
PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
PI WPI: 2001-602746/68.
XX P-PSDB; AAU29164.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX Claim 2; Fig 281; 774pp; English.
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX Sequence 1731 BP; 369 A; 592 C; 425 G; 345 T; 0 other;
SQ Query Match 73.9%; Score 1342.8; DB 22; Length 1731;
Best Local Similarity 97.7%; Pred No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCCTCTGGGACTAATACATGCGCTGCTGGAGCCACGATGT 483
DB 320 TGGGACTCGCGCTCTGCTGCTCCCTGGACTCCACGCTCGAGCCGCCACGATGT 379
QY 484 TTGCTCTTTTCCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCA CCCCCTACTTGGAGC 543
DB 380 TCTGCTTTTTCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCA CCCCCTACTTGGAGC 439

544 CACAGGCTGTGATGCTGCTGCTGTACCTGTCTCAGAGGGGCGCCATGTGAGTTGT 603
Ob CACAGGCTGTGATGCTGCTGCTGTACCTGTCTCAGAGGGGCGCCATGTGAGTTGT 499
2Y ACAGCTTCACATGTCGGCTGTCCAGTGGCCCGCAGCTGTGAGGAGCCACAGCAATGCT 663
Db ACCGCTTCACATGTCGGCTGTCCAGTGGCCCGCAGCTGTGAGGAGCCACAGCAATGCT 559
2Y GTCCAAAGTGTGTGAAAGCTCAACTCCCTCTGGAGCTCCGGGCGCCCAACAAAGTCTGCC 723
Db GTCCAAAGTGTGTGAAAGCTCAACTCCCTCTGGAGCTCCGGGCGCCCAACAAAGTCTGCC 619
2Y AGCAACAGGGAACCAATGTACCAACACGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCGCT 783
Ob AGCAACAGGGAACCAATGTACCAACACGAGAGATCTTCAGTGGCCCATGAGCTGTTCCCGCT 679
784 CCCGCTGCCACAGTGTGCTCTGTGAGCTGTGACAGAGGGCCAGATCTACTCGGCCC 843
Db CCCGCTGCCACAGTGTGCTCTGTGAGCTGTGACAGAGGGCCAGATCTACTCGGCCC 739
844 TCACAACTCCGCCCGAACGAGCTGTGCCAGCAGCCCTCCGCTGCCAGATCTGCTGCC 903
Db TCACAACTCCGCCCGAACGAGCTGTGCCAGCAGCCCTCCGCTGCCAGATCTGCTGCC 799
904 AAGCCTCCAAAGATGAGGCAAGTGAAGCAATCGATGAAGAGCAAGTGTGAGTCTGCC 963
Db AAGCCTCCAAAGATGAGGCAAGTGAAGCAATCGATGAAGAGCAAGTGTGAGTCTGCC 859
964 ATGGGCTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGCTGGAGAAAGAGAGGCCGG 1023
Db ATGGGCTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGCTGGAGAAAGAGAGGCCGG 919
1024 GCACCCAGCCCCCAGCTGCTCAGCGCCCTCTGAGCTTCTCCCTCGCATCTTCAGC 1083
Db GCACCCAGCCCCCAGCTGCTCAGCGCCCTCTGAGCTTCTCCCTCGCATCTTCAGC 979
1084 CCAAGGAGAGCAGCAGACACTGTGAAGATCTCTGAGGAGAGAAATAGAAAGCT 1143
Db CCAAGGAGAGCAGCAGACACTGTGAAGATCTCTGAGGAGAGAAATAGAAAGCT 1039
1144 GTGTGCTATGCGCGGAGAGACTCTCCACGGGAGAGTGTGGACCCCGGCTTCCGTGCT 1203
Db GTGTGCTATGCGCGGAGAGACTCTCCACGGGAGAGTGTGGACCCCGGCTTCCGTGCT 1099
1204 TCGGCCCCCTTGCCTCTATGCACTGTGAGATGGCGGAGAGTGTGGACCCCGGCTG 1263
Db TCGGCCCCCTTGCCTCTATGCACTGTGAGATGGCGGAGAGTGTGGACCCCGGCTG 1159
1264 TGACCTGTCTCAGAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db TGACCTGTCTCAGAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
1324 AGATTGCTCCAGAGGCAAGCAGACCTCTGCACTGAGTATGATGATGATGATGATGATG 1383
Db AGATTGCTCCAGAGGCAAGCAGACCTCTGCACTGAGTATGATGATGATGATGATGATG 1279
1384 CCAAGGCAACCGGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
Db CCAAGGCAACCGGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1339
1444 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1503
Db GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1399
1504 TAAAGATGAGGAAATGAGGCTCAGAGAGTGAATGATGATGATGATGATGATGATGATG 1563
Db TAAAGATGAGGAAATGAGGCTCAGAGAGTGAATGATGATGATGATGATGATGATGATG 1459
1564 AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAG 1623
Db AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAG 1519
1624 CAGCACTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683

Db 1520 CAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1579
QY 1684 ACCCTGGAGCTGAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
Db 1580 ACCCTGGAGCTGAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1639
QY 1744 AACAGTTGAGATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1803
Db 1640 AACAGTTGAGATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1699
QY 1804 CATTAACCATCAAAA 1817
Db 1700 CATTAACCATCAAAA 1713
RESULT 8
AAA37064
ID AAA37064 standard; cDNA; 1732 BP.
AC AAA37064;
XX AC
XX 08-AUG-2000 (first entry)
DX Human FRO1557 (UNQ765) cDNA sequence SEQ ID NO:141.
DE Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
KW ss.
XX Homo sapiens.
OS WO200012708-A2.
FN 09-MAR-2000.
PD
XX 01-SEP-1999; 99WO-US20111.
XX 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 15-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100651.
PR 16-SEP-1998; 98US-0100652.
PR 16-SEP-1998; 98US-0100654.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.


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18-SEP-1998; 98US-0101014.
18-SEP-1998; 98US-0101068.
18-SEP-1998; 98US-0101071.
22-SEP-1998; 98US-0101279.
23-SEP-1998; 98US-0101471.
23-SEP-1998; 98US-0101472.
23-SEP-1998; 98US-0101474.
23-SEP-1998; 98US-0101475.
23-SEP-1998; 98US-0101476.
23-SEP-1998; 98US-0101477.
23-SEP-1998; 98US-0101479.
24-SEP-1998; 98US-0101738.
24-SEP-1998; 98US-0101741.
24-SEP-1998; 98US-0101743.
24-SEP-1998; 98US-0101915.
24-SEP-1998; 98US-0101916.
24-SEP-1998; 98US-0102107.
29-SEP-1998; 98US-0102240.
29-SEP-1998; 98US-0102307.
29-SEP-1998; 98US-0102330.
29-SEP-1998; 98US-0102331.
30-SEP-1998; 98US-0102484.
30-SEP-1998; 98US-0102487.
30-SEP-1998; 98US-0102570.
30-SEP-1998; 98US-0102571.
01-OCT-1998; 98US-0102684.
01-OCT-1998; 98US-0102687.
02-OCT-1998; 98US-0102965.
06-OCT-1998; 98US-0103258.
06-OCT-1998; 98US-0103449.
07-OCT-1998; 98US-0103314.
07-OCT-1998; 98US-0103315.
07-OCT-1998; 98US-0103328.
07-OCT-1998; 98US-0103395.
07-OCT-1998; 98US-0103396.
07-OCT-1998; 98US-0103401.
08-OCT-1998; 98US-0103633.
08-OCT-1998; 98US-0103678.
08-OCT-1998; 98US-0103711.
08-OCT-1998; 98US-0104257.
20-OCT-1998; 98US-0104987.
20-OCT-1998; 98US-0105000.
20-OCT-1998; 98US-0105002.
21-OCT-1998; 98US-0105104.
22-OCT-1998; 98US-0105169.
22-OCT-1998; 98US-0105266.
26-OCT-1998; 98US-0105693.
26-OCT-1998; 98US-0105694.
27-OCT-1998; 98US-0105807.
27-OCT-1998; 98US-0105881.
27-OCT-1998; 98US-0105882.
28-OCT-1998; 98US-0106062.
28-OCT-1998; 98US-0106029.
28-OCT-1998; 98US-0106030.
28-OCT-1998; 98US-0106032.
28-OCT-1998; 98US-0106033.
28-OCT-1998; 98US-0106178.
29-OCT-1998; 98US-0106248.
29-OCT-1998; 98US-0106384.
29-OCT-1998; 98US-0106390.
03-NOV-1998; 98US-0106484.
03-NOV-1998; 98US-0106856.
03-NOV-1998; 98US-0106902.
03-NOV-1998; 98US-0106905.
03-NOV-1998; 98US-0106919.
03-NOV-1998; 98US-0106932.
03-NOV-1998; 98US-0106934.
10-NOV-1998; 98US-0107783.
17-NOV-1998; 98US-0108775.
17-NOV-1998; 98US-0108779.
17-NOV-1998; 98US-0108787.

17-NOV-1998; 98US-0108788.
17-NOV-1998; 98US-0108801.
17-NOV-1998; 98US-0108802.
17-NOV-1998; 98US-0108806.
17-NOV-1998; 98US-0108807.
17-NOV-1998; 98US-0108867.
17-NOV-1998; 98US-0108925.
18-NOV-1998; 98US-0108848.
18-NOV-1998; 98US-0108849.
18-NOV-1998; 98US-0108850.
18-NOV-1998; 98US-0108851.
18-NOV-1998; 98US-0108852.
18-NOV-1998; 98US-0108858.
18-NOV-1998; 98US-0108904.

( GETH ) GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI
XX
XX
DR WPI; 2000-237871/20.
DR P-PSDB; AAY99382.
XX
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
PS Claim 2; Fig 85; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide and receptor small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

Query Match 73.9%; Score 1342.8; DB 21; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCTCTCTGGGACTAACTAGGACTGTGGTGGTTTCCAGAGCCACAGCATGT 483
Db 321 TGGGACTCGCGTGTCTGTGTTCCCGCTGGACTCCAGCTCGAGCGCCGCGCCAGCATGT 380
QY 484 TCTGCCTTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGACCCCTACTTGGAGC 543
Db 381 TCTGCCTTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGACCCCTACTTGGAGC 440
QY 544 CACAGGCGCTGATGTACTTGTCTGCTGCTGTACTGCTCAGAGGGCGCCCACTGTAGTGT 603
Db 441 CACAGGCGCTGATGTACTTGTCTGCTGCTGTACTGCTCAGAGGGCGCCCACTGTAGTGT 500
QY 604 ACCGCTCTCACTGTCCCGCTGTCTCACTGCCCGCCAGCTGTGACGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCTCACTGTCCCGCTGTCTCACTGCCCGCCAGCTGTGACGGAGCCACAGCAATGCT 560
QY 664 GTCCGAGTGTGGAGACCTCACACTCCCTGTGAGCTCCGGGCCCGCCACCAAGTCCCTGCC 723
Db 561 GTCCCAAGTGTGGAGACCTCACACTCCCTGTGAGCTCCGGGCCCGCCACCAAGTCCCTGCC 620
QY 724 AGCAACACGGAGCCATGTATCAACACAGGAGAGATCTTTCAGTGCCCATGAGCTGTCCCT 783
Db 621 AGCAACACGGAGCCATGTATCAACACAGGAGAGATCTTTCAGTGCCCATGAGCTGTCCCT 680
QY 784 CCGGCTGCCCAACCAAGTGTGTCTCTGTGAGCTGTGAGAGGGCCAGATCTACTGCGGCC 843
Db 681 CCGGCTGCCCAACCAAGTGTGTCTCTGTGAGCTGTGAGAGGGCCAGATCTACTGCGGCC 740
QY 844 TCACAACCTGCCCGAGACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCCTGCTGCC 903

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Db	741	TCACAACTGCCCCGACCAACGAGTGGCCAGCACTCCCACTCCAGACTCTCTGCTGC	XX
Qy	904	AAGCTCTCAAGATGAGGCAAGTGAACAATCGATGAAGAGACAGTGTGCTGCTCC	DT
Db	801	AAGCTCTCAAGATGAGGCAAGTGAACAATCGATGAAGAGACAGTGTGCTGCTCC	DE
Qy	964	ATGGGGTGAGACATCTCAGATCCATGTTTCCAGTATGCTGGGAAAGAGAGGCCGG	XX
Db	861	ATGGGGTGAGACATCTCAGATCCATGTTTCCAGTATGCTGGGAAAGAGAGGCCGG	XX
Qy	1024	GCACCCAGCCCCCACTGGCTCTCAGCGCCCTCTGAGCTTTCATCCCTGCGCACTTCAGAC	OS
Db	921	GCACCCAGCCCCCACTGGCTCTCAGCGCCCTCTGAGCTTTCATCCCTGCGCACTTCAGAC	XX
Qy	1084	CCAAGGAGCAGCAGCACAACCTGCTCAAGATCGCTGAAGGAGAAACATAGAAGGCT	XX
Db	981	CCAAGGAGCAGCAGCACAACCTGCTCAAGATCGCTGAAGGAGAAACATAGAAGGCT	XX
Qy	1144	GTGTGATGTCGGGGAAGACTACTCCACCGGAGAGTGTGGACCCGCTTCCTGCT	PR
Db	1041	GTGTGATGTCGGGGAAGACTACTCCACCGGAGAGTGTGGACCCGCTTCCTGCT	PR
Qy	1204	TCGGCCCTTTGCCCTGCACTCTATGCACTCTGAGGATGGCCGCGAGGATGCGCAGCGTG	PR
Db	1101	TCGGCCCTTTGCCCTGCACTCTATGCACTCTGAGGATGGCCGCGAGGATGCGCAGCGTG	PR
Qy	1264	TGACTGTGCCACCGAGTACCCCTGCCGTCACTCCCGAGAAAGTGGTGGAAAGTGTGCA	PR
Db	1161	TGACTGTGCCACCGAGTACCCCTGCCGTCACTCCCGAGAAAGTGGTGGAAAGTGTGCA	XX
Qy	1324	AGATTGCCAGAGGAGAAAGCAAGCTGGCCACAGTGAATCAGTTCTACCAAGTGTG	XX
Db	1221	AGATTGCCAGAGGAGAAAGCAAGCTGGCCACAGTGAATCAGTTCTACCAAGTGTG	XX
Qy	1384	CAAAGGCAACCGGCGCGGCTCTGTCACACATCGGTATCCCAAGCCCAAGCACTGTC	DR
Db	1281	CAAAGGCAACCGGCGCGGCTCTGTCACACATCGGTATCCCAAGCCCAAGCACTGTC	DR
Qy	1444	GTGCGTTTGGCCCTGGAAACACGAGGCGCTCGGACTTGGTGAGATCTACTCTGGAAGCTGG	PT
Db	1341	GTGCGTTTGGCCCTGGAAACACGAGGCGCTCGGACTTGGTGAGATCTACTCTGGAAGCTGG	PT
Qy	1504	TAAAGATGAGGAACTGAGGCTCAGAGGTGAAGTCACTGGCCCAAGCCACACAGCC	PS
Db	1401	TAAAGATGAGGAACTGAGGCTCAGAGGTGAAGTCACTGGCCCAAGCCACACAGCC	XX
Qy	1564	AGAACTTCCACTTGACTCAGATCAAGAAAGTGAAGACAGACTTCCAGAAAGAGCA	CC
Db	1461	AGAACTTCCACTTGACTCAGATCAAGAAAGTGAAGACAGACTTCCAGAAAGAGCA	CC
Qy	1624	CAGCACTTCCGACTGCTCGCTGGCCCGACGAGGCTCACTGGAAGCTTCTTAGCCGAG	CC
Db	1521	CAGCACTTCCGACTGCTCGCTGGCCCGACGAGGCTCACTGGAAGCTTCTTAGCCGAG	XX
Qy	1684	ACCTGAGCTGAAGTCAAGGCTCAGACAAAGTGAAGTCAAGACATAACAAAGACT	Query Match
Db	1581	ACCTGAGCTGAAGTCAAGGCTCAGACAAAGTGAAGTCAAGACATAACAAAGACT	Best Local Similarity
Qy	1744	ACAGTTCAGATATGAGCTGTATATTTGTTATATATATATATATATATATATATATATAT	Matches 1362; Conservative
Db	1641	ACAGTTCAGATATGAGCTGTATATTTGTTATATATATATATATATATATATATATATAT	0; Mismatches 32; Indels 0; Gaps 0;
Qy	1804	CATAACCATCAAAA 1817	424 TTGGGCTGGAGCTCTGGGACTAACAATGCACTGCTCGGTTTGCAGGCCACAGACATGT 483
Db	1701	CATTACCTCAAAA 1714	321 TGGAGCTGCGCTGCTCTGTTCCCTCGACTCCCACTGAGCCCGCCACAGATGT 380

RESULT 9
AAF92098
ID AAF92098 standard; cDNA: 1732 BP.
XX
AC AAF92098;

15-MAY-2001 (first entry)
Human PRO1557 cDNA.
Human; PRO protein; mapping; ss.
Homo sapiens.
MO200116318-A2.
08-MAR-2001.
24-AUG-2000; 2000WO-US23328.
01-SEP-1999; 99MO-US20111.
15-SEP-1999; 99MO-US21090.
07-DEC-1999; 99US-0169495.
09-DEC-1999; 99US-0170262.
11-JAN-2000; 2000US-0175481.
18-FEB-2000; 2000MO-US04341.
18-FEB-2000; 2000MO-US04342.
22-FEB-2000; 2000MO-US04414.
01-MAR-2000; 2000MO-US05601.
03-MAR-2000; 2000US-0187202.
25-APR-2000; 2000US-0199397.
22-MAY-2000; 2000MO-US14042.
05-JUN-2000; 2000US-0209832.
(GETH) GENENTECH INC.
Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
MPI; 2001-183260/18.
P-PSDB; AAB87566.
Eighty four nucleic acids encoding PRO polypeptides, useful in
molecular biology, including use as hybridization probes, and in
chromosome and gene mapping. -
Claim 2; Fig 81; 278pp; English.
The present sequence is the coding sequence for a human PRO polypeptide
(secreted and transmembrane). The PRO protein, and PRO agonists, PRO
antagonists or anti-PRO antibodies are useful for preparation of a
medicament useful in the treatment of a condition which is responsive to
the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
protein may also be employed as molecular weight markers for protein
electrophoresis. The PRO coding sequence has applications in molecular
biology, including use as hybridisation probes, and in chromosome and
gene mapping.
Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;
Query Match 73.9%; Score 1342.8; DB 22; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGGCTGGAGCTCTGGGACTAACAATGCACTGCTCGGTTTGCAGGCCACAGACATGT 483
Db 321 TGGAGCTGCGCTGCTCTGTTCCCTCGACTCCCACTGAGCCCGCCACAGATGT 380
Qy 484 TCTGCTTTTCCATGGAGAGATACCTCCCGGCGAGAGCTGGCACCCTTACTTGGAGC 543
Db 381 TCTGCTTTTCCATGGAGAGATACCTCCCGGCGAGAGCTGGCACCCTTACTTGGAGC 440
Qy 544 CACAAGGCTGTATGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
Db 441 CACAAGGCTGTATGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
Qy 604 ACCGCTTCCACTGTCCGCTTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663

501	ACGCGCTCCAC	TGTGCCCTGTGTC	CACTGTCGCCCGAGCGCTGTG	ACGCGAGCCAC	CAGCAATGCT	560	
664	GTCCCAAGTGT	TGGAAACCTCA	CACTCCCTCTGGA	CTCGGGGCCCCCA	CAAAAGTCTGCTGCC	723	
561	GTCCCAAGTGT	TGGAACTCA	CACTCCCTCTGGA	CTCGGGGCCCCCA	CAAAAGTCTGCTGCC	620	
724	AGCACAAACGGG	ACATGTACCA	ACGAGAGAGATCTT	TCAGTGGCCCATG	AGCTGTTCCTCCT	783	
621	AGCACAAACGGG	ACCATGTACCA	ACGAGAGAGATCTT	CAGTGGCCCATG	AGCTGTTCCTCCT	680	
784	CCGCGCTGCC	CAACCACTGTGCT	CTCCTCAGCTG	CGCAAGAGGGCGAGATCT	ACTACGGCGC	843	
681	CCGCGCTGCC	CAACCACTGTGCT	CTCCTCAGCTG	CGCAAGAGGGCGAGATCT	ACTACGGCGC	740	
844	TCAACACCTG	CCCCGAAACAG	GGCTGGCCAGACCCCT	CCCGCTGGCCAGATCT	CTCTGCTGCTC	903	
741	TCACAACTG	CCCCGAAACAG	GGCTGGCCAGACCCCT	CCCACTGCCAGATCT	CTCTGCTGCTC	800	
904	AAGCCTGTCAA	AAGTAGGCGCAAGT	TGAGCAATCGGAT	GAAAGGACAGTGT	CGCATGCGCTCC	963	
801	AAGCCTGTCAA	AAGTAGGCGCAAGT	TGAGCAATCGGAT	GAAAGGACAGTGT	CGCATGCGCTCC	860	
964	ATGGGGTGA	GACATCCTCAG	AGATTCATGCT	TGGGAGAAAGAGAGCGCCGG		1023	
861	ATGGGGTGA	GACATCCTCAG	AGATTCATGCT	TGGGAGAAAGAGAGCGCCGG		920	
1024	GCACCCCG	CCCCCACTGG	CGCTCAGGGCCCTCT	TGAGCTTCACTCCCTCG	CCACTTCAGAC	1083	
921	GCACCCCG	CCCCCACTGG	CGCTCAGGGCCCTCT	TGAGCTTCACTCCCTCG	CCACTTCAGAC	980	
1084	CCAAAGGAG	CGAGGACACAACT	TGTCATAGATGCT	TGAAAGGAGAAACAT	TAAGAAAGCCT	1143	
981	CCAAAGGAG	CGAGGACACAACT	TGTCATAGATGCT	TGAAAGGAGAAACAT	TAAGAAAGCCT	1040	
1144	GTGTGCA	TGGCGGGAAG	CACTACTCCAC	CGGGAGGTGTGGCA	CCCGGCTCTCCGTGCTC	1203	
1041	GTGTGCA	TGGCGGGAAG	CACTACTCCAC	CGGGAGGTGTGGCA	CCCGGCTCTCCGTGCTC	1100	
1204	TCGGCCCC	TGCGCTG	CATCTATG	CACTGTGAGGATGG	CGCGCAGGATGCGCAGAGCTG	1263	
1101	TCGGCCCC	TGCGCTG	CATCTATG	CACTGTGAGGATGG	CGCGCAGGATGCGCAGAGCTG	1160	
1264	TGACCTGT	CCCCACGAGT	ACCGCTGCGCT	CAACCCGAGAAAGTGGCT	GGGAGTCTGCTGCA	1323	
1161	TGACCTGT	CCCCACGAGT	ACCGCTGCGCT	CAACCCGAGAAAGTGGCT	GGGAGTCTGCTGCA	1220	
1324	AGATTG	CCGCAAGGACAA	AGACCTTGGCC	CAAGTGAATCATGTTCTT	TACCAAGTGTCT	1383	
1221	AGATTG	CCGCAAGGACAA	AGACCTTGGCC	CAAGTGAATCATGTTCTT	TACCAAGTGTCT	1280	
1384	CCAAAGG	CACCGGGCGCG	GGTCTCTG	CTCCACATCGGTAT	CCCAAGCGCCAGCAACCTGCG	1443	
1281	CCAAAGG	CACCGGGCGCG	GGTCTCTG	CTCCACATCGGTAT	CCCAAGCGCCAGCAACCTGCG	1340	
1444	GTCCCTTT	CGCTTGGAA	CACAGGCGCT	CGGACTTGGTGGAGATCT	TACCTCTGGAAGCTGG	1503	
1341	GTCCCTTT	CGCTTGGAA	CACAGGCGCT	CGGACTTGGTGGAGATCT	TACCTCTGGAAGCTGG	1400	
1504	TAAAGAT	GAGGAAATCG	AGGCTCAGAGAGGT	GAGTACCTTGGCCCAAGGCC	CACACAGCC	1563	
1401	TAAAGAT	GAGGAAATCG	AGGCTCAGAGAGGT	GAGTACCTTGGCCCAAGGCC	CACACAGCC	1460	
1564	AGAACTTT	CGACTTGA	CTCAGATCAAGAAAGT	CAAGAACCAAGACTT	TCGAAGAGGCA	1623	
1461	AGAACTTT	CGACTTGA	CTCAGATCAAGAAAGT	CAAGAACCAAGACTT	TCGAAGAGGCA	1520	
1624	CAGCACTT	CCGACTGCT	GCTGGCCGCCCA	CGAAGGTCACTT	CGGAAGCTCTTCTTACGCCAG	1683	
1521	CAGCACTT	CCGACTGCT	GCTGGCCGCCCA	CGAAGGTCACTT	CGGAAGCTCTTCTTACGCCAG	1580	
1684	ACCTTGAG	GTGAAGGTCA	CGGGCCAGT	TCAGA	CAAAAGTGA	CCCAAGCATTAACAAAGACCT	1743
1581	ACCTTGAG	GTGAAGGTCA	CGGGCCAGT	TCAGA	CAAAAGTGA	CCCAAGCATTAACAAAGACCT	1640

	QY	1744	AACAGTTGCAGATGAGCTGTATAAATTGGTTCATTATATTAATTAATAGAAGTTG	1800	
	DB	1641	AACAGTTGCAGATGAGCTGTATAAATTGGTTCATTATATTAATTAATAGAAGTTG	1700	
	QY	1804	CATAACCCTCAAAA 1817 		
	DB	1701	CATTACCCTCAAAA 1714 		
	RESULT 10				
	ID AAF54300	standard; DNA; 1732 BP.			
	XX AC AAF54300;				
	DT DT 02-APR-2001	(first entry)			
	DE DE DNA encoding protein of the invention #43.				
	KW KW Secreted; transmembrane; gene therapy; ss.				
	OS OS Unidentified.				
	PX PX WO200007961-A1.				
	PN PN 28-DEC-2000.				
	PD PD 18-FEB-2000; 2000WO-US04342.				
	PF PF 23-JUN-1999; 99US-0141037.				
	PX PR 20-JUL-1999; 99US-0144758.				
	PR PR 26-JUL-1999; 99US-0145698.				
	PR PR 01-SEP-1999; 99WO-US20111.				
	PR PR 29-OCT-1999; 99US-0162506.				
	PR PR 30-NOV-1999; 99WO-US28313.				
	PR PR 02-DEC-1999; 99WO-US28551.				
	PR PR 16-DEC-1999; 99WO-US30095.				
	PR PR 05-JAN-2000; 2000WO-US00219.				
	PR PR 06-JAN-2000; 2000WO-US00376.				
	PA PA (GETH) GENENTECH INC.				
	PI PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S; PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AU, Hillan KJ, PI Pan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tumas D; PI Watanabe CK, Williams PM, Wood WI; PX WPI; 2001-071395/08. Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene therapy - Claim 2; Fig 85; 787pp; English. The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy. Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other; Query Match 73.9%; Score 1342.8; DB 22; Length 1732; Best Local Similarity 97.7%; Pred.No. 0; Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0; QY 424 TTGGCCTCGAGCCCTCTGGACTAAACATGCCACTGGTGCTTTGCCAGGCCAGCATGT 483 DB 321 TGGAACATCGCGTGTCTGGTTCTCCCTGGACTCCCACGCTCGAGCCGCCAGCATGT 380				

2Y 484 TCTGCTTTTCCATCGGGAAGAGATATCTCCCGCGGAGAGCTGCGACCCCTACTTGGAGC 543
Db 381 TCTGCTTTTCCATCGGGAAGAGATATCTCCCGCGGAGAGCTGCGACCCCTACTTGGAGC 440
2Y 544 CACAAGGCTGTGATCTGCTGCGCTGTACCTGTCTGAGAGGCGCCCACTGTGAGTGTGT 603
Db 441 CACAAGGCTGTGATCTGCTGCGCTGTACCTGTCTGAGAGGCGCCCACTGTGAGTGTGT 500
2Y 604 ACCGCTCCACATGTCCGCTGTCCACTGCGCCCGCAGCTGTGAGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCCACATGTCCGCTGTCCACTGCGCCCGCAGCTGTGAGGAGCCACAGCAATGCT 560
2Y 664 GTCCCAAGTGTGGAACCTCAGCTCCCTCTGGAATCCGGGCCCAACCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACCTCAGCTCCCTCTGGAATCCGGGCCCAACCAAGTCTCTGCC 620
2Y 724 AGCAACAACGGGACCATGTACCAACAACGAGAGATCTTCAAGTGCCCATGAGCTGTTCCCTC 783
Db 621 AGCAACAACGGGACCATGTACCAACAACGAGAGATCTTCAAGTGCCCATGAGCTGTTCCCTC 680
2Y 784 CCCGCTGCCCAACAGTGTCTCTGCACTGCGCCCGCAGCTGACAGAGGCGCAGATCTACTCGGCCC 843
Db 681 CCCGCTGCCCAACAGTGTCTCTGCACTGCGCCCGCAGCTGACAGAGGCGCAGATCTACTCGGCCC 740
2Y 844 TCACAACCTGCCCGAACCGAGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCGAACCGAGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 800
2Y 904 AAGCTCGAAGATGAGGAGTGAAGATCGAGATCGGATGAGAGACAGTGTGAGTGTCTCC 963
Db 801 AAGCTCGAAGATGAGGAGTGAAGATCGAGATCGGATGAGAGACAGTGTGAGTGTCTCC 860
2Y 964 ATGGGGTGAGACATCTCAGAGATCATGTGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 1023
Db 861 ATGGGGTGAGACATCTCAGAGATCATGTGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 920
2Y 1024 GCACCCAGCCCCCATCTGCTGAGCTGAGCGCCCTCTGAGCTTATCCCTGCGCATCTCAGAC 1083
Db 921 GCACCCAGCCCCCATCTGCTGAGCTGAGCGCCCTCTGAGCTTATCCCTGCGCATCTCAGAC 980
2Y 1084 CCAAGGAGAGAGCAGCAGACATCTGCAAGATCTCTGAGGAGAAACATTAAGAAAGCT 1143
Db 981 CCAAGGAGAGAGCAGCAGACATCTGCAAGATCTCTGAGGAGAAACATTAAGAAAGCT 1040
2Y 1144 GTGTGCTATGGCGGGAAGACGTACTCCCAACGCGGAGAGTGTGGCACCCCGGCTTCCGTGCT 1203
Db 1041 GTGTGCTATGGCGGGAAGACGTACTCCCAACGCGGAGAGTGTGGCACCCCGGCTTCCGTGCT 1100
2Y 1204 TCGGCCCTTGCCTCATCTATGCACTGTGAGATGCGCGCCAGGACTGCGACGCTG 1263
Db 1101 TCGGCCCTTGCCTCATCTATGCACTGTGAGATGCGCGCCAGGACTGCGACGCTG 1160
2Y 1264 TGACCTGTCCACGAGTACCTCGCTGACCCCGCAGAAAGTGGCTGGAGTGTCTGCA 1323
Db 1161 TGACCTGTCCACGAGTACCTCGCTGACCCCGCAGAAAGTGGCTGGAGTGTCTGCA 1220
2Y 1324 AGATTGCCCAGAGGACAAAGCAGACCTGGCCACAGTGAATCAGTTCTACACAGTGTCT 1383
Db 1221 AGATTGCCCAGAGGACAAAGCAGACCTGGCCACAGTGAATCAGTTCTACACAGTGTCT 1280
2Y 1384 CCAAGGACACCGGCGCGGCTCTGCTCCACATCGGTATCCCGACAGCCACAGCAACCTGC 1443
Db 1281 CCAAGGACACCGGCGCGGCTCTGCTCCACATCGGTATCCCGACAGCCACAGCAACCTGC 1340
2Y 1444 GTCGCTTTGCTGGAACACGAGGCTCGGACTTGTGGAGATCTACCTCTGGAAGCTGG 1503
Db 1341 GTCGCTTTGCTGGAACACGAGGCTCGGACTTGTGGAGATCTACCTCTGGAAGCTGG 1400
2Y 1504 TAAAGATGAGAAATCTGAGGCTCAGAGAGTGAAGTACTGCGCCCAAGGCGCACAGCC 1563
Db 1401 TAAAGATGAGAAATCTGAGGCTCAGAGAGTGAAGTACTGCGCCCAAGGCGCACAGCC 1460

QY 1564 AGAATCTTCCACTTCACTGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGAGGCA 1623
Db 1461 AGAATCTTCCACTTCACTGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGAGGCA 1520
QY 1624 CAGCACTTCGCACTGCTCGCTGGCCCCCAAGAGTCACTGGAACGCTTCTTCCAGCCAG 1683
Db 1521 CAGCACTTCGCACTGCTCGCTGGCCCCCAAGAGTCACTGGAACGCTTCTTCCAGCCAG 1580
QY 1684 ACCCTGGAGCTGAAGGTCAOCCGCCAGTCCAGACAAGAGTGAACCAAGAGCACT 1743
Db 1581 ACCCTGGAGCTGAAGGTCAOCCGCCAGTCCAGACAAGAGTGAACCAAGAGCACT 1640
QY 1744 AACAGTTGACAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAAGAGTTG 1803
Db 1641 AACAGTTGACAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAAGAGTTG 1700
QY 1804 CATTAACCATCAAAA 1817
Db 1701 CATTAACCATCAAAA 1714
RESULT 11
ABS74418
ID ABS74418 standard; cDNA; 1732 BP.
XX ABS74418;
AC ABS74418;
XX
XX
DT 10-DEC-2002 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO1557.
XX
XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
XX
XX antirheumatic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
KW
XX
XX Homo sapiens.
XX
XX US2002119130-A1.
XX
XX 29-AUG-2002.
XX
XX 06-DEC-2001; 2001US-0006867.
XX
XX 29-OCT-1997; 97US-063435P.
XX 29-OCT-1997; 97US-064215P.
PR 22-APR-1998; 98US-082797P.
PR 29-APR-1998; 98US-083495P.
PR 15-MAY-1998; 98US-085579P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 11-JUN-1998; 98US-088863P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089514P.
PR 16-SEP-1998; 98WO-US19330.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21194.
PR 22-DEC-1999; 99WO-US30720.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 30-MAR-2000; 2000WO-US08439.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32378.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.

20-JUN-2001; 2001WO-US19692.
29-JUN-2001; 2001WO-US21066.
09-JUL-2001; 2001WO-US21735.
(GETH) GENENTECH INC.
Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
I Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
X WPI; 2002-731348/79.
R P-PSDB; ABG95891.
X
R New isolated secreted and transmembrane PRO polypeptide useful for
T modulating biological activity of a cell, or for treating
I sports-related joint problems, osteoarthritis or rheumatoid arthritis
X
S Claim 2; Fig 81; 399pp; English.
X
C The invention relates to an isolated secreted and transmembrane PRO
C polypeptide having 80 % sequence identity to a sequence appearing
C as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
C an extracellular domain of the proteins with their associated signal
C peptide or lacking its associated signal peptide. Also included are
C the nucleic acids encoding the proteins, vectors, host cells,
C fusion proteins and antibodies which specifically bind to the proteins.
C The proteins are useful for detecting a polypeptide designated as A, B, C
C or D in a sample suspected of containing an A, B, C or D polypeptide,
C by contacting the sample with a polypeptide designated as E, F, G, H or
C I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
C or D/I polypeptide conjugate in the sample, where the formation of the
C conjugate is indicative of the presence of an A, B, C or D polypeptide
C in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
C polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
C E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
C polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
C polypeptide. The sample comprises a cell suspected of expressing the A,
C B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
C a detectable label or is attached to a solid support. The proteins are
C useful for linking a bioactive molecule to a cell expressing a
C polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
C molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
C causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
C against them are useful for modulating a biological activity of a cell
C expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
C I. The cell is killed. The proteins are useful for identifying
C agonists or antagonists for the preparation of a medicament useful in
C the treatment of a condition which is responsive to the proteins, as
C molecular weight markers for protein electrophoresis purposes, and as
C therapeutic agents for treating sports-related joint problems,
C articular cartilage defects, osteoarthritis or rheumatoid arthritis.
C Nucleic acids encoding the proteins are useful as hybridisation probes,
C in chromosome and gene mapping, in the generation of anti-sense RNA and
C DNA, for the preparation of the proteins, to generate transgenic or
C knockout animals which are useful in the development and screening of
C therapeutic useful reagents, for chromosome identification, and in gene
C therapy. The antibody is useful as a therapeutic agent, in a diagnostic
C assay and for affinity purification of the protein from recombinant
C cell culture natural sources. The present sequence encodes a novel
C secreted or transmembrane protein of the invention.
X
X Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

QY	544	CACAAGGCGCTGATGTACTGCTGCGCTGTACTGCTTACAGAGGCGCCCATGTGAGTTGTT	603
DB	441	CACAAGGCGCTGATGTACTGCTGCGCTGTACTGCTTACAGAGGCGCCCATGTGAGTTGTT	500
QY	604	ACGGCTCTCCACTGTCGGCGCTGTCCACTGCGCCCGAGCTGTGACGAGGCCACAGCAATGCT	663
DB	501	ACGGCTCTCCACTGTCGGCGCTGTCCACTGCGCCCGAGCTGTGACGAGGCCACAGCAATGCT	560
QY	664	GTCCCAAGTGTGTGGAACCTCACAATCCCTCTGGAATCCGGGCCCCCAACAAAGTCTCTGCC	723
DB	561	GTCCCAAGTGTGTGGAACCTCACAATCCCTCTGGAATCCGGGCCCCCAACAAAGTCTCTGCC	620
QY	724	AGCAACAAGGAGCATGTATCAACACGAGAGATCTTCAGTGCCTCCATGAGTGTTCCTCT	783
DB	621	AGCAACAAGGAGCATGTATCAACACGAGAGATCTTCAGTGCCTCCATGAGTGTTCCTCT	680
QY	784	CCGGCTCTCCCAACCAAGTGTGTCTTCTGACCTGCAGAGGCGCCAGATCTACTGCGGCC	843
DB	681	CCGGCTCTCCCAACCAAGTGTGTCTTCTGACCTGCAGAGGCGCCAGATCTACTGCGGCC	740
QY	844	TCACAACTCTGCCCGCAACACGAGCTGCCAGCAACCTTCCGGTGGCAGATCTCTGTCTGCC	903
DB	741	TCACAACTCTGCCCGCAACACGAGCTGCCAGCAACCTTCCGGTGGCAGATCTCTGTCTGCC	800
QY	904	AAGCTCTCAAAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTGTCTGCC	963
DB	801	AAGCTCTCAAAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTGTCTGCC	860
QY	964	ATGGGGTGAAGACATCTCTCAGGATCCATGTCTCAGTGTGAGGAGAAAGAGAGGCCGG	1023
DB	861	ATGGGGTGAAGACATCTCTCAGGATCCATGTCTCAGTGTGAGGAGAAAGAGAGGCCGG	920
QY	1024	GCACCCGAGCCCGACCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
DB	921	GCACCCGAGCCCGACCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980
QY	1084	CAAGGGAGAGGAGGAGCAAACTGTGAAGATGCTCTGAAGAGAGAAACATTAAGAAAGCCT	1143
DB	981	CAAGGGAGAGGAGGAGCAAACTGTGAAGATGCTCTGAAGAGAGAAACATTAAGAAAGCCT	1040
QY	1144	GTGTGATGCGGGGGAAGAGCTACTCTCCACGGGGAGGTGTGGCAACCGCCCTTCCTGTCCT	1203
DB	1041	GTGTGATGCGGGGGAAGAGCTACTCTCCACGGGGAGGTGTGGCAACCGCCCTTCCTGTCCT	1100
QY	1204	TCGGCCCTTGGCTGCTGATCTATGAGTGTGAGGAGTGGCGGAGGAGTGTGGCAACCGCCCT	1263
DB	1101	TCGGCCCTTGGCTGCTGATCTATGAGTGTGAGGAGTGGCGGAGGAGTGTGGCAACCGCCCT	1160
QY	1264	TGACCTGTCCCGAGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1323
DB	1161	TGACCTGTCCCGAGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1220
QY	1324	AGATTGTCCTCCAGAGGCAAAAGCAGACCTCTGCGCAAGTGTGATGATGATGATGATGATG	1383
DB	1221	AGATTGTCCTCCAGAGGCAAAAGCAGACCTCTGCGCAAGTGTGATGATGATGATGATGATG	1280
QY	1384	CCAAGGACACCGGGCGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1443
DB	1281	CCAAGGACACCGGGCGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1340
QY	1444	GTGGCTTTGCTTGGGACAGAGGCTCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1503
DB	1341	GTGGCTTTGCTTGGGACAGAGGCTCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1400
QY	1504	TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGAGGCCACAGGCC	1563
DB	1401	TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGAGGCCACAGGCC	1460
QY	1564	AGAAATCTTCCATTTGATCAGATCAAGAAAGTCAAGAGCAAGATCTTCCAGAAAGAGGCA	1623
DB	1461	AGAAATCTTCCATTTGATCAGATCAAGAAAGTCAAGAGCAAGATCTTCCAGAAAGAGGCA	1520

Y	424	TTGGGCTGAGCCCTCTGGGACTTAACATGGCACTGTGGTTCGGTTCAGGCGCCAGACATGT	483
b	321	TGGGACTGCGCTGCTGCTGCTTCCCGCTGGACTCCCAAGCTGAGCGCGCCAGACATGT	380
Y	484	TCTGCTTTTCCATGGAAGAGATATCTCCCGCGGAGAGCTGGCACCCCTTCTGGAGC	543
b	381	TCTGCTTTTCCATGGAAGAGATATCTCCCGCGGAGAGCTGGCACCCCTTCTGGAGC	440

Query Match	73.9%	Score 1342.8;	DB 24;	Length 1732;
Best local similarity	97.7%	Pred. No. 0;		
Matches 1362;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0;

2Y 1624 CAGCACTTCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAACTCTTCTTACCCAG 1583
Db 1521 CAGCACTTCGACTGCTCGCTGGCCCCCAGCAAGGTCACTGGAACTCTTCTTACCCAG 1580
2Y 1684 ACCCTGAGCTGAAGGTCAACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAGACCT 1743
Db 1581 ACCCTGAGCTGAAGGTCAACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAGACCT 1640
2Y 1744 AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATTAATTAAATAAAGAGTTG 1803
Db 1641 AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATTAATTAAATAAAGAGTTG 1700
2Y 1804 CATACCACTCAAA 1817
Db 1701 CATACCACTCAAA 1714

RESULT 12

ACA57823

ID ACA57823 standard; cDNA; 1732 BP.

XX AC

ACA57823;

AC

10-JUN-2003 (first entry)

DT

XX

Human PRO1557 cDNA.

DE

XX

KW Human; PRO; secreted; transmembrane; cytotstatic; TNF-alpha; blood; gene;

KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;

KW differentiation; tumour; Gene therapy; ss.

XX

OS Homo sapiens.

XX

US2003036143-A1.

PN

XX

20-FEB-2003.

PD

XX

02-JUL-2002; 2002US-0187600.

PF

XX

16-SEP-1998; 98WO-US219330.

PR

07-OCT-1998; 98WO-US21141.

PR

01-DEC-1998; 98WO-US25108.

PR

08-MAR-1999; 99WO-US05028.

PR

14-MAY-1999; 99WO-US10733.

PR

02-JUN-1999; 99WO-US12252.

PR

01-SEP-1999; 99WO-US20111.

PR

15-SEP-1999; 99WO-US21090.

PR

01-DEC-1999; 99WO-US28301.

PR

02-DEC-1999; 99WO-US28551.

PR

30-DEC-1999; 99WO-US31274.

PR

05-JAN-2000; 2000WO-US00219.

PR

18-FEB-2000; 2000WO-US04341.

PR

18-FEB-2000; 2000WO-US04342.

PR

22-FEB-2000; 2000WO-US04414.

PR

24-FEB-2000; 2000WO-US05004.

PR

01-MAR-2000; 2000WO-US05601.

PR

02-MAR-2000; 2000WO-US05841.

PR

15-MAR-2000; 2000WO-US06884.

PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 11-DEC-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 17-DEC-1997; 97US-069425P.
PR 18-DEC-1997; 97US-069870P.
PR 10-MAR-1998; 97US-068017P.
PR 11-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 20-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 26-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.

Query Match		73.9%	Score 1342.8;	DB 25;	Length 1732;
Best Local Similarity		97.7%	Fred. No. 0;		
Matches 1362;		Conservative	0;	Mismatches	32;
				Indels	0;
				Gaps	0;
QY	424	TTGGGCTGAGCTCTCGGAGCTAAACATGGCACTGGTCGGTTTGCAGGCCAGACATGT	483		
DB	321	TGGGACTCGCGTCTGTGGTTCCCTCGACTCCACGCTCGAGCCGCCAGACATGT	380		
QY	484	TCGCGCTTTTCCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	543		
DB	381	TCGCGCTTTTCCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC	440		
QY	544	CACAAGGCTGATGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	603		
DB	441	CACAAGGCTGATGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	500		
QY	604	ACGCGCTCCACTGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	663		
DB	501	ACGCGCTCCACTGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	560		
QY	664	GTCCCAAGTGTGGAACTTACCAACGAGAGATCTTCAGTGGCCCAACCAAGTCTCTGCC	723		
DB	561	GTCCCAAGTGTGGAACTTACCAACGAGAGATCTTCAGTGGCCCAACCAAGTCTCTGCC	620		
QY	724	AGCACAACGGAGACCATGTACCAACGAGAGATCTTCAGTGGCCCAACCAAGTCTCTGCC	783		
DB	621	AGCACAACGGAGACCATGTACCAACGAGAGATCTTCAGTGGCCCAACCAAGTCTCTGCC	680		
QY	784	CCGCGCTGCCAAACGAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	843		
DB	681	CCGCGCTGCCAAACGAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	740		
QY	844	TCACAACTTGCCTCGAACAGGCTGCCAGACCCCTCCGCTGCTGCTGCTGCTGCTGCTGCT	903		
DB	741	TCACAACTTGCCTCGAACAGGCTGCCAGACCCCTCCGCTGCTGCTGCTGCTGCTGCTGCT	800		
QY	904	AAGCTTGCAAAAGATGAGGCAAGTGAAGCAATCGATGGAAGAGGACAGTGTGCAAGTGCCT	963		
DB	801	AAGCTTGCAAAAGATGAGGCAAGTGAAGCAATCGATGGAAGAGGACAGTGTGCAAGTGCCT	860		
QY	964	ATGGGTGAGACATCTTCAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1023		
DB	861	ATGGGTGAGACATCTTCAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	920		
QY	1024	GCAACCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1083		
DB	921	GCAACCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	980		
QY	1084	CCAAGGAGCAGGAGCAGCAACCTGTCAAGATCGTCTGGAAGAGAAACATAAGAAAGCCT	1143		
DB	981	CCAAGGAGCAGGAGCAGCAACCTGTCAAGATCGTCTGGAAGAGAAACATAAGAAAGCCT	1040		
QY	1144	GTGTGATGCGGGAAGACGTACTCCACGCGGAGGTGTGSCACCCGCTTCCGCTGCT	1203		
DB	1041	GTGTGATGCGGGAAGACGTACTCCACGCGGAGGTGTGSCACCCGCTTCCGCTGCT	1100		
QY	1204	TCGCGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1263		
DB	1101	TCGCGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1160		
QY	1264	TGACCTGTCCCAACCGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1323		
DB	1161	TGACCTGTCCCAACCGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1220		
QY	1324	AGATTTTCCAGAGCAAAAGCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1383		
DB	1221	AGATTTTCCAGAGCAAAAGCAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1280		
QY	1384	CCAAGGACCGGCGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1443		
DB	1281	CCAAGGACCGGCGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1340		

RESULT 13	
ACA58850	
ID	ACA58850 standard; cDNA; 1732 BP.
XX	
AC	ACA58850;
XX	
AC	
XX	
DDT	10-JUN-2003 (first entry)
XX	
DE	cDNA encoding human secreted polypeptide PRO1557.
XX	
DE	Human; ss; gene; gene therapy; tumour; cancer.
XX	
KW	
OS	Homo sapiens.
XX	
XX	
PN	US2003013855-A1.
XX	
PD	16-JAN-2003.
XX	
PF	03-MAY-2002; 2002US-0063616.
XX	
PR	30-DEC-1998; 98KR-0062142.
PR	08-MAR-1999; 99WO-US05028.
PR	14-MAY-1999; 99WO-US10733.
PR	30-DEC-1999; 99WO-US31274.
PR	18-FEB-2000; 2000WO-US04341.
PR	01-MAR-2000; 2000WO-US05601.
PR	02-MAR-2000; 2000WO-US05841.
PR	21-MAR-2000; 2000WO-US07532.
PR	22-MAY-2000; 2000WO-US10402.
PR	02-JUN-2000; 2000WO-US15264.
PR	24-AUG-2000; 2000WO-US23328.
PR	10-NOV-2000; 2000WO-US30873.
PR	01-DEC-2000; 2000WO-US32678.
PR	20-DEC-2000; 2000WO-US34956.
PR	28-FEB-2001; 2001WO-US06520.
PR	01-JUN-2001; 2001WO-US17800.
PR	14-MAY-1999; 99US-0311832.
PR	25-AUG-1999; 99US-0360137.
PR	25-AUG-1999; 99US-0360138.
PR	25-AUG-1999; 99US-0360139.
PR	25-AUG-1999; 99US-0360142.
PR	15-SEP-1999; 99US-0397342.
PR	18-OCT-1999; 99US-0403297.
PR	12-NOV-1999; 99US-0423844.

Seq	Sequence	1732 BP	369 A	592 C	425 G	346 T	0 other	
Query Match	73.9%	Score	1342.8	DB	25	Length	1732	
Best Local Similarity	97.7%	Pred.	No. 0					
Matches 1362	Conservative	0	Mismatches	32	Indels	0	Gaps	0
QY	424	TTGGGCTGGAGCCTCTCGTGACTAA	CATGCGACTGTGTCGGTTTGCAGGCGCCACAGATCT	483				
Db	321	TGGGACTCGCGTGTCTGTGTCTTCCCTCGACTCCACGCTCGAGCGCCGCCACAGATCT	380					
QY	484	TCTGCTTTTCCATGCGAAGAGATACTCCCGCGGAGAGCTGGCACCCCTACTCTTGAGGC	543					
Db	381	TCTGCTTTTCCATGCGAAGAGATACTCCCGCGGAGAGCTGGCACCCCTACTCTTGAGGC	440					
QY	544	CACAAAGCCTGATGTACTGCTCGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTTGTT	603					
Db	441	CACAAAGCCTGATGTACTGCTCGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTTGTT	500					
QY	604	ACCGCTCCCACTGTCCGGCTGTGTCACGTGCCGCCAGCTGTGACGGAGGCCACAGCAATGCT	663					
Db	501	ACCGCTCCCACTGTCCGGCTGTGTCACGTGCCGCCAGCTGTGACGGAGGCCACAGCAATGCT	560					
QY	664	GTCCCAAGCTGTGGAACCTCACTACCTCTCTGACTCTCCGGGCCCCACCAAGTCTCTGCC	723					
Db	561	GTCCCAAGCTGTGGAACCTCACTACCTCTCTGACTCTCCGGGCCCCACCAAGTCTCTGCC	620					

[illegible]

D6			1701 CATTACCTCAAAA	1714
RESULT 14				
ACA60403				
ID	ACA60403		standard; cDNA; 1732 BP.	
AC	ACA60403;			
CC				
DT	11-JUN-2003	(first entry)		
DD				
DE	Novel human secreted and transmembrane			
DX	Human; secreted and transmembrane			
KW	chromosome mapping; gene mapping; therapeutic agent screening; chromo-			
KW	somal mapping; gene therapy.			
OS	Homo sapiens.			
SS				
US	US2003018183-A1.			
FN				
PD	23-JAN-2003.			
PF				
PP	01-MAY-2002; 2002US-0063512.			
PR	06-DEC-2001; 2001US-0006867.			
PA	(GETH) GENENTECH INC.			
PI	Eaton DL, Filvaroff E, Gerritsen			
FI	Grimaldi JC, Gurney AL, Watanabe			
DR	WPI; 2003-330984/31.			
XX	P-FSDB; ABU71992.			
DD				
PT	New secreted and transmembrane PRO			
PT	molecules encoding the polypeptide			
PT	preparing a medicament for treating			
PT	the PRO polypeptide or antibody			
XX				
PS	Disclosure; Fig 81; 409pp; English			
CC	The invention describes novel iso-			
CC	polypeptides or anti-PRO antibodies			
CC	for treating a condition that is			
CC	antibody. The PRO nucleotide sequ-			
CC	ences in chromosome and gene map-			
CC	ping and DNA. PRO nucleic acids are			
CC	in assays to identify other process-			
CC	es, to generate transgenic			
CC	turn are useful in the development			
CC	of reagents, for chromosome i-			
CC	PRO polypeptides and nucleic acid			
CC	therapy, and as molecular weight			
CC	purposes. The anti-PRO antibodies			
CC	PRO, or for the affinity purification			
CC	culture or natural sources. This			
CC	secreted and transmembrane PRO po-			
XX				
SQ	Sequence 1732 BP; 369 A; 592 C; 4			
	Query Match	73.9%	Score	
	Best Local Similarity	97.7%	Produce	
	Matches 1362; Conservative	0; M		
QY	424 TTGGCGTGGAGCCTCTGGACTATTA			
Db	321 TGGAGCTGGCGCTGCTGTGGTGTC			
QY	484 TTGCCTTTTCCAATGGGAAGAGAT			

Db	1701 CATTACCTCAAAA 1714	
RESULT 14		
ACA60403		
ID	ACA60403 standard; cDNA; 1732 BP.	
XX	ACA60403;	
XX	11-JUN-2003 (first entry)	
XX	Novel human secreted and transmembrane protein PRO1557 cDNA.	
XX	Human; secreted and transmembrane polypeptide; gene; ss	
XX	chromosome mapping; gene mapping; transgenic animal; knockout animal;	
XX	therapeutic agent screening; chromosome identification; tissue typing;	
XX	gene therapy.	
XX	Homo sapiens.	
XX	US2003018193-A1.	
XX	23-JAN-2003.	
XX	01-MAY-2002; 2002US-0063512.	
XX	06-DEC-2001; 2001US-0006967.	
XX	(GETH) GENENTECH INC.	
XX	Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PU;	
XX	Grimaldi JC, Gurney AI, Watanabe CK, Wood WI;	
XX	WPI; 2003-330984/31.	
XX	P-FSDH; ABU71992.	
XX	New secreted and transmembrane PRO polypeptides and nucleic acid	
XX	molecules encoding the polypeptides, useful in gene therapy or	
XX	preparing a medicament for treating a condition that is responsive to	
XX	the PRO polypeptide or antibody	
XX	Disclosure; Fig 81; 409pp; English.	
XX	The invention describes novel isolated PRO polypeptides. The PRO	
XX	polypeptides or anti-PRO antibodies are useful in preparing a medicament	
XX	for treating a condition that is responsive to the PRO polypeptide or	
XX	antibody. The PRO nucleotide sequences may be used as hybridisation	
XX	probes in chromosome and gene mapping, or in generating antisense RNA	
XX	and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,	
XX	in assays to identify other proteins or molecules involved in binding	
XX	reaction, to generate transgenic animals or knockout animals, which in	
XX	turn are useful in the development and screening of therapeutically	
XX	useful reagents, for chromosome identification, and tissue typing. The	
XX	PRO polypeptides and nucleic acid molecules are also useful in gene	
XX	therapy, and as molecular weight markers for protein electrophoresis	
XX	purposes. The anti-PRO antibodies may be used in diagnostic assays for	
XX	PRO, or for the affinity purification of PRO from recombinant cell	
XX	culture or natural sources. This sequence encodes a novel human	
XX	secreted and transmembrane PRO polypeptide.	
XX	Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;	
XX	Query Match 73.9%; Score 1342.8; DB 25; Length 1732;	
XX	Best Local Similarity 97.7%; Pred. No. 0;	
XX	Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;	
Qy	424 TTGGGCTGGAGCTCTCTGGGACTAACATGGCACTGGTCGGTTGCGAGCCGACATCT 483	
Db	321 TGGGACTCGCGTGCCTCTGGTTCCTCCGCTCCGAGCTCGAGCCGCCGACATGT 380	
Qy	484 TCTGCTTTTTCATGGGAGAGATACTCCCCCGGAGAGCTGGCACTCTTGAGC 543	

381 TCTGCTTTTCCATGGAAGAGATATCTCCCTCCGCGAGAGCTGGGACCCCTACTTGGAGC 440
Db
544 CACAAGGCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGGGCCCATGTGAGTTGTT 603
Qy
441 CACAAGGCTGATGTACTGCTGCGCTGTACTCTGCTCAGAGGGGCCCATGTGAGTTGTT 500
Db
604 ACCGCTTCCACTGCTGCGCTGTGCACTGCGCCCGAGGCTGTGACGAGGACACAGCAATGCT 663
Qy
501 ACCGCTTCCACTGCTGCGCTGTGCACTGCGCCCGAGGCTGTGACGAGGACACAGCAATGCT 560
Db
664 GTTCCAGATGTGGAACTCAGCTCCCTCTGCACTCCGCGGCCCCACCAAGTCTCTGCC 723
Qy
561 GTTCCAGATGTGGAACTCAGCTCCCTCTGCACTCCGCGGCCCCACCAAGTCTCTGCC 620
Db
724 AGCACAAGGACCATGTATCAACACGAGAGATCTTCACTGCCCATGAGCTGTTCCCTT 783
Qy
621 AGCACAAGGACCATGTATCAACACGAGAGATCTTCACTGCCCATGAGCTGTTCCCTT 680
Db
784 CCGGCTGCCCCAACCACTGTGCTCTCTGCACTGCAAGAGGGCCAGATCTACTGCGGC 843
Qy
681 CCGGCTGCCCCAACCACTGTGCTCTCTGCACTGCAAGAGGGCCAGATCTACTGCGGC 740
Db
844 TCACAACTGCGCCGAAACAGAGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 903
Qy
741 TCACAACTGCGCCGAAACAGAGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 800
Db
904 AAGCTGCAAGATGAGGCAAGTGAAGCATCGATGAAGAGACAGTGTGAGTCTGCTCC 963
Qy
801 AAGCTGCAAGATGAGGCAAGTGAAGCATCGATGAAGAGACAGTGTGAGTCTGCTCC 860
Db
964 ATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCGG 1023
Qy
861 ATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCGG 920
Db
1024 GCACCCAGCCCCACTGCGCTCAGCGGCCCTCTGAGAGCTTCATCCCTCGCCACTTCAGAC 1083
Qy
921 GCACCCAGCCCCACTGCGCTCAGCGGCCCTCTGAGAGCTTCATCCCTCGCCACTTCAGAC 980
Db
1084 CCAAGGAGAGCAGCAGCAATGTCTCAGATCTGCTGAGGAGAAACATGAAGAAAGCTT 1143
Qy
981 CCAAGGAGAGCAGCAGCAATGTCTCAGATCTGCTGAGGAGAAACATGAAGAAAGCTT 1040
Db
1144 GTGTGATGCGGGAGAGAGTATCTCCACGGGAGGTGTGGACCCGCCCTTCGTTGCTT 1203
Qy
1041 GTGTGATGCGGGAGAGAGTATCTCCACGGGAGGTGTGGACCCGCCCTTCGTTGCTT 1100
Db
1204 TCGGCCCTTGGCTGATCTCTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGGGTG 1263
Qy
1101 TCGGCCCTTGGCTGATCTCTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGGGTG 1160
Db
1264 TGACCTGTCCACCGAGTACCCCTGCTGACCCCGAGAAAGTGTGGAGAGTGTGCA 1323
Qy
1161 TGACCTGTCCACCGAGTACCCCTGCTGACCCCGAGAAAGTGTGGAGAGTGTGCA 1220
Db
1324 AGATTGGCCAGAGAGCAAGAGAGCCCTTGGCCACAGTGATCAGTGTCTACAGGNGTC 1383
Qy
1221 AGATTGGCCAGAGAGCAAGAGAGCCCTTGGCCACAGTGATCAGTGTCTACAGGNGTC 1280
Db
1384 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCGACCAACTGTC 1443
Qy
1281 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCGACCAACTGTC 1340
Db
1444 GTCCCTTGGCTTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1503
Qy
1341 GTCCCTTGGCTTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1400
Db
1504 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1563
Qy
1401 TAAAGATGAGAACTGAGGCTCAGAGAGGTGAAGTACTGCGCCCAAGGCCACACAGCC 1460
Db
1564 AGAATCTTCCATCTGATCTAGATCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1623
Qy
1461 AGAATCTTCCATCTGATCTAGATCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1520
Db

1624 CAGCACTTCGACTGCTGCTGGCCCCCAGGAAGTCACTGGAAGCTTCTCTAGCCAG 1683
Qy
1521 CAGCACTTCGACTGCTGCTGGCCCCCAGGAAGTCACTGGAAGCTTCTCTAGCCAG 1580
Db
1684 ACCCTGAGCTGAAGTCAAGGCCAGTCCAGACAAAAGTCAAGACATACAAAGACCT 1743
Qy
1581 ACCCTGAGCTGAAGTCAAGGCCAGTCCAGACAAAAGTCAAGACATACAAAGACCT 1640
Db
1744 AACAGTTGCAGATATGAGCTGTATAATTTGTTTATATATATATATAAATAAAGAGTTG 1803
Qy
1641 AACAGTTGCAGATATGAGCTGTATAATTTGTTTATATATATATATAAATAAAGAGTTG 1700
Db
1804 CATACCATCAAA 1817
Qy
1701 CATACCATCAAA 1714
Db

RESULT 15
ACA63413

ID ACA63413 standard; cDNA; 1732 BP.

XX ACA63413;

XX 13-JUN-2003 (first entry)

XX cDNA encoding human PRO polypeptide #41.

XX Human; PRO polypeptide; secreted and transmembrane protein;
XX anti-PRO antibody; diagnostic assay; gene expression; gene; ss.

XX Homo sapiens.

XX US2003023042-A1.

XX 30-JAN-2003.

XX 01-MAY-2002; 2002US-0063502.

XX 06-DEC-2001; 2001US-0006867.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PU;

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-331484/31.

XX P-ESDE; ABU72149.

XX Novel monoclonal antibody that binds to secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and
PT also for treating conditions responsive to the antibody -

XX Disclosure; Fig 81; 408pp; English.

XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The
XX PRO polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a
XX medicament useful in the treatment of a condition responsive to
XX anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
XX assays for PRO, by detecting its expression in specific cells,
XX tissues or serum, and for affinity purification of PRO from
XX recombinant cell culture or natural sources. ACA63373-ACA63456
XX represent cDNA sequences encoding the human PRO polypeptides of
XX the invention.

XX Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;

XX Query Match 73.9%; Score 1342.8; DB 25; Length 1732;

XX Best Local Similarity 97.7%; Pred. No. 0;

XX Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

424 TTGGCTGGAGCTCTCTGGGACTAATGSCACTGGTGGTTTGGCCAGGCCACAGACATGT 483
321 TGGGACTCGCGCTCTCTGTCTGTTCCCTCTGGACTCTCCACGGCTCGAGAGCCGCCACAGACATGT 380
484 TCTGCTCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACCTCTACTTTGGAGC 543
381 TCTGCTCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACCTCTACTTTGGAGC 440
544 CACAAGGCTGATGATCTGCTGCTGGCTGTACTGTCTCAGAGGGGCCCAATGAGTTGTT 603
441 CACAAGGCTGATGATCTGCTGCTGGCTGTACTGTCTCAGAGGGGCCCAATGAGTTGTT 500
604 ACAGCTTCCACTGTCCGCTCTCCACTGCCCCCAGCCTGTGACGAGGCCACACAGCAATGCT 663
501 ACAGCTTCCACTGTCCGCTCTCCACTGCCCCCAGCCTGTGACGAGGCCACACAGCAATGCT 560
664 GTCCCAAGTGTGTGAACCTCACACTCTCTGGAATCTCCGGGCCCCACAAAGTCTCTGCC 723
561 GTCCCAAGTGTGTGAACCTCACACTCTCTGGAATCTCCGGGCCCCACAAAGTCTCTGCC 620
724 AGCACAAGGGAACCATGTACCAACAGGGAGAGATCTTCAAGTGCCCATGAGCTGTCCCT 783
621 AGCACAAGGGAACCATGTACCAACAGGGAGAGATCTTCAAGTGCCCATGAGCTGTCCCT 680
784 CCGCTGTGCCCAACCAAGTGTCTCTGTGAGTGTGCACAGAGGGCCAGATCTACTGGGCC 843
681 CCGCTGTGCCCAACCAAGTGTCTCTGTGAGTGTGCACAGAGGGCCAGATCTACTGGGCC 740
844 TCACAACCTGTCCCGCCGAAACAGGCTGCCCCAGCAACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903
741 TCACAACCTGTCCCGCCGAAACAGGCTGCCCCAGCAACCCCTCCCGCTGCCAGACTCTCTGCTGCC 800
904 AAGCTGCAAGATGAGCAAGTGTGAGCAATCGGATGAGAGGAGCAGTGTGAGTGCCTCC 963
801 AAGCTGCAAGATGAGCAAGTGTGAGCAATCGGATGAGAGGAGCAGTGTGAGTGCCTCC 860
964 ATGGGGTGAACATCTCAGATCCATGTTTCCAGTGTGTCGAGAGAGAGAGAGGCCCGG 1023
861 ATGGGGTGAACATCTCAGATCCATGTTTCCAGTGTGTCGAGAGAGAGAGAGGCCCGG 920
1024 GCACCCAGCCGCCCACTGGCTCAGGCGCCCTCTGAGCTTCATCCCTCGCCCACTTCAGAC 1083
921 GCACCCAGCCGCCCACTGGCTCAGGCGCCCTCTGAGCTTCATCCCTCGCCCACTTCAGAC 980
1084 CCAAGGAGCAGGCAAGCAACTGTCAAGATCGTCTCAAGGAGAACATAAGAAAGCT 1143
981 CCAAGGAGCAGGCAAGCAACTGTCAAGATCGTCTCAAGGAGAACATAAGAAAGCT 1040
1144 GTGTGATGGCGGAGAGAGCTACTCCACGGGAGGTGTGGCACCCGGCTTCGGTGCCT 1203
1041 GTGTGATGGCGGAGAGAGCTACTCCACGGGAGGTGTGGCACCCGGCTTCGGTGCCT 1100
1204 TCGGCCCTTGGCCCTGCATCTATGCACTGTGAGGATGGCGCCAGGACTGCCAGCGTG 1263
1101 TCGGCCCTTGGCCCTGCATCTATGCACTGTGAGGATGGCGCCAGGACTGCCAGCGTG 1160
1264 TGACCTGTCCCAACCGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAGTGTCTGCA 1323
1161 TGACCTGTCCCAACCGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAGTGTCTGCA 1220
1324 AGATTTTCCCAAGGAGCAAGAGACCTTGGCCACAGTGTGATCAGTTCTTCCAGGTGTC 1383
1221 AGATTTTCCCAAGGAGCAAGAGACCTTGGCCACAGTGTGATCAGTTCTTCCAGGTGTC 1280
1384 CCAAGGACCGGGCCGGGTCTCTGTCCACACATTCGGTATCCCCAAGCCCAAGCACTTGC 1443
1281 CCAAGGACCGGGCCGGGTCTCTGTCCACACATTCGGTATCCCCAAGCCCAAGCACTTGC 1340
1444 CTCGCTTTGGCCCTTGGAAACACAGGCGCTTCGAGCTTGGTGGAGATCTACTCTTGGAAAGTGG 1503
1341 CTCGCTTTGGCCCTTGGAAACACAGGCGCTTCGAGCTTGGTGGAGATCTACTCTTGGAAAGTGG 1400
1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTTGGGCCCAAGGCCACACAGCC 1563

Db 1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACTCTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCCACTTCACTCAGATCAAGAAAGTCAGAAAGTCAGAAAGAGGCA 1623
Db 1461 AGAATCTTCCACTTCACTCAGATCAAGAAAGTCAGAAAGTCAGAAAGAGGCA 1520
Qy 1624 CAGCACTTCCGACTGCTGCTGGCCCCCAGCAAGTGTCTGGAAGCTTCTTCCAGCCAG 1683
Db 1521 CAGCACTTCCGACTGCTGCTGGCCCCCAGCAAGTGTCTGGAAGCTTCTTCCAGCCAG 1580
Qy 1684 ACCCTGAGCTCAAGGTCAACGGCCAGTTCAGCAAAAGTGAACAAAGACCT 1743
Db 1581 ACCCTGAGCTCAAGGTCAACGGCCAGTTCAGCAAAAGTGAACAAAGACCT 1640
Qy 1744 AACAGTTGTCAGATATGAGCTGTATAATTTGTTTATTATATTAATAAAGAGTTG 1803
Db 1641 AACAGTTGTCAGATATGAGCTGTATAATTTGTTTATTATATTAATAAAGAGTTG 1700
Qy 1804 CATTAACCATCAAA 1817
Db 1701 CATTAACCATCAAA 1714

RESULT 16
ABX98293
ID ABX98293 standard; cDNA; 1732 BP.
XX
XX ABX98293;
AC
AC
DT 19-MAY-2003 (first entry)
XX
XX Human cDNA encoding a secreted/transmembrane protein, SEQ ID 281.
XX
XX Human; ss; gene; PRO; secreted protein; transmembrane protein;
XX cytosolic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX cervical tumour; liver tumour; TNF-alpha release; arthritis;
XX tumour necrosis factor alpha; chondrocyte cell; bone disorder;
XX cartilage disorder; sports injury.
XX
XX Homo sapiens.
XX
XX US2003036156-A1.
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XX 20-FEB-2003.
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XX 02-JUL-2002; 2002US-0188767.
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XX 16-SEP-1998; 98WO-US19330.
XX 07-OCT-1998; 98WO-US21141.
XX 01-DEC-1998; 98WO-US25108.
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XX 14-MAY-1999; 99WO-US10733.
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XX 02-MAR-2000; 2000WO-US05641.
XX 15-MAR-2000; 2000WO-US06884.
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XX 22-MAY-2000; 2000WO-US14042.
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381	TTCTGCTTTTCCATGGGNAAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC	440
544	CACAGGCTGTATGTATGCTGCTGGTGTACCTGTCTAGAGGGCGCCATGTGAGTTGTT	603
441	CACAGGCTGTATGTATGCTGCTGGTGTACCTGTCTAGAGGGCGCCATGTGAGTTGTT	500
604	ACCGCTCTCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCT	663
501	ACCGCTCTCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCT	560
664	GTCCCAAGTGTGGGAACCTCACACTCCCTCTGGACTCCGGGCCCCCACCAGTCTCTGCC	723
561	GTCCCAAGTGTGGGAACCTCACACTCCCTCTGGACTCCGGGCCCCCACCAGTCTCTGCC	620
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621	AGCAGAGGGGACATGTACACACAGGAGATCTTCAGTCCCATGAGCTGTCCCT	680
784	CCGCTGTCGCAACAGTGTGTCTGTGAGCTGTGACAGAGGAGCCAGATCTACTGCGCC	843
681	CCGCTGTCGCAACAGTGTGTCTGTGAGCTGTGACAGAGGAGCCAGATCTACTGCGCC	740
844	TCACAACTTGCCCGGACCCAGGCTGCGGACACCCCTCCCGCTGCGCAGACTCTCTGCTGCC	903
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861	ATGGGTGAGACATCTCAGATTCATGTTCAGTGTATGCTGGGAAAGAGAGGCCCGG	920
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921	GCACCCAGCCGACCTGGCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTTTCAGAC	980
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XX	gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;	
XX	adrenal tumour; lung tumour; colon tumour; breast tumour;	
XX	prostate tumour; rectal tumour; cervical tumour; liver tumour;	
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XX	US2003036157-A1.	
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XX	02-JUL-2002; 2002US-0198769.	
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PR 29-JUN-2001; 2001WO-US21066.
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b 381 TCTGCTTTTCCATGGGAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTTGGAGC 440
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b 561 GTCCCAAGTGTGGAACTCTCACTCTCCCTGTGAGCTCCGGGCCCCCACCAGGTCCTGGCC 620
Y 724 AGCACACGGGACCACTGTACCAACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 783
b 621 AGCACACGGGACCACTGTACCAACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 680
Y 784 CCGGCTGCCCAACGAGTGTGCTCTCTGAGCTGCACAGGGGCCAGATCTACTGGGGCC 843
b 681 CCGGCTGCCCAACGAGTGTGCTCTCTGAGCTGCACAGGGGCCAGATCTACTGGGGCC 740
Y 844 TCACAACCTGCCCGAAACAGGCTGCCAGACCCCTCCCGTGTGCAGACTCTGTGTGCC 903
b 741 TCACAACCTGCCCGAAACAGGCTGCCAGACCCCTCCCGTGTGCAGACTCTGTGTGCC 800
Y 904 AAGCTTGAAGATGAGGCAAGTGAAGCAATCGGATGAAGGACAGTGTGAGTGTGCTCC 963
b 801 AAGCTTGAAGATGAGGCAAGTGAAGCAATCGGATGAAGGACAGTGTGAGTGTGCTCC 860
Y 964 ATGGGGTGAAGATCTCAGGATCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
b 861 ATGGGGTGAAGATCTCAGGATCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
Y 1024 GCACCCGAGCCCACTGTGGCTGTAGGCCCCCTCTGAGCTTCACTGCTCCGACTTCAGAC 1083
b 921 GCACCCGAGCCCACTGTGGCTGTAGGCCCCCTCTGAGCTTCACTGCTCCGACTTCAGAC 980
Y 1084 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCTGCTTGAAGGAGAAACATAAGAAAGCCT 1143
b 981 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCTGCTTGAAGGAGAAACATAAGAAAGCCT 1040
Y 1144 GTGTGATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCCCTTCGCTGCT 1203

Db 1041 GTGTGATGGCGGGAAGACGTACTCCACGGGAGGTGTGGCACCCGGCTTCGTGCCT 1100
Qy 1204 TGGGCCCCCTTGGCTTGCATCTCTATGCACTCTGTGAGGATGCGCCGAGACTTGGCAGGCTG 1263
Db 1101 TGGGCCCCCTTGGCTTGCATCTCTATGCACTCTGTGAGGATGCGCCGAGACTTGGCAGGCTG 1160
Qy 1264 TGAACCTGTCACCCGAGTACCCCTGCGCTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA 1323
Db 1161 TGACCTGTGCCACCGAGTACCCCTGCGCTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA 1220
Qy 1324 AGATTTTGGCCAGAGGACAAAGCAGACCCCTGGCCCACTGAGATCAGTTCTACCAAGTGTGTC 1383
Db 1221 AGATTTTGGCCAGAGGACAAAGCAGACCCCTGGCCCACTGAGATCAGTTCTACCAAGTGTGTC 1280
Qy 1384 CCAAGGACCCGGGCGGGTCTCTCGTCCACATCGGTATCCCGCAGCCAGCAACCTGC 1443
Db 1281 CCAAGGACCCGGGCGGGTCTCTCGTCCACATCGGTATCCCGCAGCCAGCAACCTGC 1340
Qy 1444 GTCCGTTTGGCCCTGGAAACAGAGGCTCGGACTCTGGTGGAGATCTACCTCTGGAGCTGG 1503
Db 1341 GTCCGTTTGGCCCTGGAAACAGAGGCTCGGACTCTGGTGGAGATCTACCTCTGGAGCTGG 1400
Qy 1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCCACTTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1623
Db 1461 AGAATCTTCCACTTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1520
Qy 1624 CAGCACTTCCGACTGCTCGCTGCGCCGCCACGAGGTCACCTGCACTGCACTGCTGCTGCTGCTGCT 1683
Db 1521 CAGCACTTCCGACTGCTCGCTGCGCCGCCACGAGGTCACCTGCACTGCACTGCTGCTGCTGCTGCT 1580
Qy 1684 ACCTGGAGCTGAAGGTCAGGCGCAGTCCAGACAAAGTGAACAGCAATACAAAGACCT 1743
Db 1581 ACCTGGAGCTGAAGGTCAGGCGCAGTCCAGACAAAGTGAACAGCAATACAAAGACCT 1640
Qy 1744 AACAGTTCACAGATGAGCTGTATAATTTGTTTATATATATATATATATATATATATATATATAT 1803
Db 1641 AACAGTTCACAGATGAGCTGTATAATTTGTTTATATATATATATATATATATATATATATATAT 1700
Qy 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714
RESULT 18
ACA05840
ID ACA05840 standard; cDNA; 1732 BP.
XX ACA05840;
AC ACA05840;
XX XX
XX 29-MAY-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #141.
DE Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX Homo sapiens.
XX US2003036162-A1.
XX 20-FEB-2003.
XX 12-JUL-2002; 2002US-0194423.
XX 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.

PR	08-MAR-1999;	99WO-US05028.	PT	markers, in tissue typing, and in chromosome identification -
PR	14-MAY-1999;	99WO-US10733.	XX	Claim 2; Fig 281; 706pp; English.
PR	02-JUN-1999;	99WO-US12252.	PS	
PR	01-SEP-1999;	99WO-US20111.	XX	
PR	15-SEP-1999;	99WO-US21090.	CC	The invention discloses human nucleic acids encoding secreted and
PR	01-DEC-1999;	99WO-US28301.	CC	transmembrane (PRO) polypeptides. Also disclosed is an antibody that
PR	02-DEC-1999;	99WO-US28551.	CC	specifically binds to the PRO polypeptide, a method for stimulating the
PR	30-DEC-1999;	99WO-US31274.	CC	release of tumour necrosis factor alpha (TNF-alpha) from human blood by
PR	05-JAN-2000;	2000WO-US00219.	CC	contacting the blood a PRO polypeptide, a method for stimulating the
PR	18-FEB-2000;	2000WO-US04341.	CC	proliferation or differentiation of chondrocyte cells by contacting the
PR	18-FEB-2000;	2000WO-US04342.	CC	cells with a PRO polypeptide, a method for detecting the presence of a
PR	22-FEB-2000;	2000WO-US04414.	CC	tumour in a mammal and an oligonucleotide probe derived from any of the
PR	24-FEB-2000;	2000WO-US05004.	CC	PRO nucleotide sequences. The nucleotide sequences are useful as
PR	01-MAR-2000;	2000WO-US05601.	CC	in chromosome and gene mapping, in generating antisense RNA and DNA, in
PR	02-MAR-2000;	2000WO-US05841.	CC	preparing PRO polypeptides by recombinant techniques and in gene therapy
PR	15-MAR-2000;	2000WO-US06884.	CC	(e.g. for replacement of defective gene). The PRO polypeptides are useful
PR	10-MAR-2000;	2000WO-US08439.	CC	as molecular weight markers for protein electrophoresis purposes, for
PR	17-MAY-2000;	2000WO-US13705.	CC	chromosome identification, as chromosome markers, as therapeutic agents,
PR	22-MAY-2000;	2000WO-US14042.	CC	for stimulating the release of TNF-alpha from human blood, for
PR	30-MAY-2000;	2000WO-US14941.	CC	stimulating the proliferation or differentiation of chondrocytes and
PR	02-JUN-2000;	2000WO-US15264.	CC	detecting the presence of a tumour. The PRO polypeptides and nucleic
PR	28-JUL-2000;	2000WO-US20710.	CC	acids may also be used diagnostically for tissue typing. The sequences
PR	24-AUG-2000;	2000WO-US22328.	CC	presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
PR	08-NOV-2000;	2000WO-US30952.	CC	polypeptides of the invention.
PR	01-DEC-2000;	2000WO-US32678.	XX	
PR	20-DEC-2000;	2000WO-US34956.	XX	Sequence 1732 BP; 369 A; 592 C; 425 G; 346 T; 0 other;
PR	28-FEB-2001;	2001WO-US06520.	QY	Query Match
PR	01-JUN-2001;	2001WO-US17800.	QY	Best Local Similarity 73.9%; Score 1342.8; DB 25; Length 1732;
PR	20-JUN-2001;	2001WO-US19692.	QY	Mismatches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
PR	29-JUN-2001;	2001WO-US21066.	Db	
PR	09-JUL-2001;	2001WO-US21735.	QY	424 TTGGGCTGGAGCTCTCGGACTAACATGCACTGTGTGGTTTCCAGGCCACAGCATGT 483
PR	29-AUG-2001;	2001WO-US27099.	Db	321 TGGGACTCGGCTGTCTGTGTTCCCTCGGACTCCACGCTCGAGCCGCGCCAGCATGT 380
PR	26-JUN-1998;	98US-0105413.	QY	484 TCTGCTTTTCCATGGGAAGAGATACCTCCCGGGAGAGCTGCACCCCTACTTGGAGC 543
PR	06-NOV-1998;	98US-0187368.	Db	381 TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGAGAGCTGCACCCCTACTTGGAGC 440
PR	07-DEC-1998;	98US-0202054.	QY	544 CACAAGGCTGATGTACTGCTGCTGCTGTACTGTCTAGAGGGCGCCCATGTGAGTTGTT 603
PR	03-MAR-1999;	99US-0254311.	Db	441 CACAAGGCTGATGTACTGCTGCTGCTGTACTGTCTAGAGGGCGCCCATGTGAGTTGTT 500
PR	14-MAY-1999;	99US-0311832.	QY	604 ACCGCTTCCACTGTGCGGCTGTCCACTGTGCGGCTGTGACGGAGCCACAGCAATGCT 663
PR	25-AUG-1999;	99US-0380137.	Db	501 ACCGCTTCCACTGTGCGGCTGTGCGGCTGTGACGGAGCCACAGCAATGCT 560
PR	25-AUG-1999;	99US-0380138.	QY	664 GTCCCAAGTGTGGAACTCAGACTCCCTCTGGAATCCGGGCGCCACCAAGTCTGCTGCC 723
PR	25-AUG-1999;	99US-0380142.	Db	561 GTCCCAAGTGTGGAACTCAGACTCCCTCTGGAATCCGGGCGCCACCAAGTCTGCTGCC 620
PR	18-OCT-1999;	99US-0403297.	QY	724 AGCAACAAGGACCATGTATACCAACAGGAGATCTTCACTGAGTGGCCCATGAGTTCCTCC 783
PR	22-AUG-2000;	2000US-0644848.	Db	621 AGCAACAAGGACCATGTATACCAACAGGAGATCTTCACTGAGTGGCCCATGAGTTCCTCC 680
PR	18-SEP-2000;	2000US-0664610.	QY	784 CCCGCTGCCCAACCAAGTGTGCTCTGTGAGTGTGACAGAGGGCCAGATCTACTCGGGCC 843
PR	18-SEP-2000;	2000US-0665350.	Db	681 CCCGCTGCCCAACCAAGTGTGCTCTGTGAGTGTGACAGAGGGCCAGATCTACTCGGGCC 740
PR	08-NOV-2000;	2000US-0709238.	QY	844 TCACAACCTGCCCGGAAACAGGCTGCCAGACCCCTCCGCTGCCAGATCTCTGCTGCC 903
PR	20-DEC-2000;	2000US-0747259.	Db	741 TCACAACCTGCCCGGAAACAGGCTGCCAGACCCCTCCGCTGCCAGATCTCTGCTGCC 800
PR	22-MAR-2001;	2001US-0816744.	QY	904 AAGCTCTCAAGATGAGGCAAGTGAAGCAATCGATGAGAGGAGAGGACAGTGTGCTGCTGCC 963
PR	10-MAY-2001;	2001US-0854208.	Db	801 AAGCTCTCAAGATGAGGCAAGTGAAGCAATCGATGAGAGGAGAGGAGTGTGCTGCTGCC 860
PR	25-MAY-2001;	2001US-0854280.	QY	964 ATGGGGTGAGACATCTCTCAGGATCCATGTTTCCAGTATGCTTGGGAGAAAGAGAGGCCCGG 1023
PR	05-JUN-2001;	2001US-0874503.	Db	861 ATGGGGTGAGACATCTCTCAGGATCCATGTTTCCAGTATGCTTGGGAGAAAGAGAGGCCCGG 920
PR	18-JUL-2001;	2001US-0908827.	QY	1024 GCACCCAGCCGCCACTGCGCTCAGCGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC 1083
PR	30-JUL-2001;	2001US-0918585.	XX	
PR	06-AUG-2001;	2001US-0924419.	XX	
PR	13-AUG-2001;	2001US-0929404.	XX	
PR	16-AUG-2001;	2001US-0931836.	XX	
PR	28-AUG-2001;	2001US-0941992.	XX	
PR	04-SEP-2001;	2001US-0946374.	XX	
PR	15-JAN-2002;	2002US-0052586.	XX	
PR	(GETH) GENENTECH INC.		XX	
PR	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;		XX	
PR	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;		XX	
PR	WPI; 2003-332039/31.		XX	
PR	P-PSDB; ABU67546.		XX	
PR	New secreted and transmembrane PRO polypeptides and nucleic acids,		XX	
PR	useful in gene therapy, in chromosome and gene mapping, as chromosome		XX	

b	921	GCACCCAGCCCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTTCAGAC	980	PD	13-FEB-2003.
Y	1084	CAAGGGAGCAGGACGACCAACTGTCTGAGATGCTCTTGAAGGAGAAACATAAGAAAGCCT	1143	XX	17-JUN-2002; 2002US-0173697.
b	981	CAAGGGAGCAGGACGACCAACTGTCTGAGATGCTCTTGAAGGAGAAACATAAGAAAGCCT	1040	XX	
Y	1144	GTGTGATGGGGGAGAACCTTACTCCCAACGGGAGGTGTGACACCGGCTTCCGTGCCT	1203	PR	16-SEP-1998; 98WO-US19330.
b	1041	GTGTGATGGGGGAGAACCTTACTCCCAACGGGAGGTGTGACACCGGCTTCCGTGCCT	1100	PR	07-OCT-1998; 98WO-US21141.
Y	1204	TGGGCCCCCTTGCCTGTGATCTGTATGCACTGTGAGATGAGATGGCCGCCAGACTGCCAGGCTG	1263	PR	01-DEC-1998; 98WO-US25108.
b	1101	TGGGCCCCCTTGCCTGTGATCTGTATGCACTGTGAGATGAGATGGCCGCCAGACTGCCAGGCTG	1160	PR	08-MAR-1999; 99WO-US05028.
Y	1264	TGACCTGTCCCAACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGGAAGTGTCTGCA	1323	PR	14-MAY-1999; 99WO-US10733.
b	1161	TGACCTGTCCCAACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGGAAGTGTCTGCA	1220	PR	02-JUN-1999; 99WO-US12252.
Y	1324	AGATTGGCCAGAGACAAAGCAGACCTCTGGCCACAGTGAGATCAAGTCTTACCAAGGTGC	1383	PR	01-SEP-1999; 99WO-US20111.
b	1221	AGATTGGCCAGAGACAAAGCAGACCTCTGGCCACAGTGAGATCAAGTCTTACCAAGGTGC	1280	PR	15-SEP-1999; 99WO-US21090.
Y	1384	CGAAGCCACCGGCGGGTCTCTGTCCACATCGGTATCCCCAAGCCCGAGACCACTGC	1443	PR	01-DEC-1999; 99WO-US28301.
b	1281	CGAAGCCACCGGCGGGTCTCTGTCCACATCGGTATCCCCAAGCCCGAGACCACTGC	1340	PR	02-DEC-1999; 99WO-US28551.
Y	1444	GTGCTTTGGCCCTGGAAACACAGGGCTCGAATTGGTGGAGATCTACCTCTGGAAGCTGG	1503	PR	30-DEC-1999; 99WO-US31274.
b	1341	GTGCTTTGGCCCTGGAAACACAGGGCTCGAATTGGTGGAGATCTACCTCTGGAAGCTGG	1400	PR	05-JAN-2000; 2000WO-US00219.
Y	1504	TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1563	PR	18-FEB-2000; 2000WO-US04341.
b	1401	TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC	1460	PR	22-MAY-2000; 2000WO-US14042.
Y	1564	AGATCTTCCATTGACTCAGATCAGAAAGTCCAGGAGCAGACCTCCAGAAAGGCA	1623	PR	30-MAY-2000; 2000WO-US14941.
b	1461	AGATCTTCCATTGACTCAGATCAGAAAGTCCAGGAGCAGACCTCCAGAAAGGCA	1520	PR	02-JUN-2000; 2000WO-US15264.
Y	1624	CAGCATTCGCACTGCTCGTGGCCGCCCAAGAGGTCACTGGAAAGTCTTCTAGCCCAAG	1683	PR	28-JUL-2000; 2000WO-US20710.
b	1521	CAGCATTCGCACTGCTCGTGGCCGCCCAAGAGGTCACTGGAAAGTCTTCTAGCCCAAG	1580	PR	24-AUG-2000; 2000WO-US23328.
Y	1684	ACCCTGGAGCTGAAGGTCACGGCAGTCCAGACAAAGTGAACCAAGACATAACAAGACCT	1743	PR	08-NOV-2000; 2000WO-US30952.
b	1581	ACCCTGGAGCTGAAGGTCACGGCAGTCCAGACAAAGTGAACCAAGACATAACAAGACCT	1640	PR	01-DEC-2000; 2000WO-US32678.
Y	1744	ACAGTTGCAGATGAGCTGATTAATTGTTGTTATTATATATTAATAAAGAGTTG	1803	PR	20-DEC-2000; 2000WO-US34956.
b	1641	ACAGTTGCAGATGAGCTGATTAATTGTTGTTATTATATTAATAAAGAGTTG	1700	PR	28-FEB-2001; 2001WO-US05520.
Y	1804	CATACCTCAAAA 1817		PR	01-JUN-2001; 2001WO-US17800.
b	1701	CATTACCTCAAAA 1714		PR	20-JUN-2001; 2001WO-US19692.
RESULT 19				PR	29-JUN-2001; 2001WO-US21066.
EX97884				PR	09-JUL-2001; 2001WO-US21735.
D	ABX97884	standard; cDNA; 1732 BP.		PR	29-AUG-2001; 2001WO-US27099.
X				PR	18-SEP-1997; 97US-052663P.
C	ABX97884;			PR	18-SEP-1997; 97US-052663P.
X				PR	21-OCT-1997; 97US-062250P.
T	16-MAY-2003 (first entry)			PR	17-OCT-1997; 97US-063486P.
X				PR	24-OCT-1997; 97US-063121P.
X				PR	24-OCT-1997; 97US-063121P.
X				PR	28-OCT-1997; 97US-063540P.
X				PR	28-OCT-1997; 97US-063541P.
X				PR	28-OCT-1997; 97US-063544P.
X				PR	28-OCT-1997; 97US-063564P.
X				PR	29-OCT-1997; 97US-063734P.
X				PR	31-OCT-1997; 97US-063870P.
X				PR	31-OCT-1997; 97US-064103P.
X				PR	13-NOV-1997; 97US-065311P.
X				PR	21-NOV-1997; 97US-066120P.
X				PR	24-NOV-1997; 97US-066466P.
X				PR	24-NOV-1997; 97US-066772P.
X				PR	11-DEC-1997; 97US-069335P.
X				PR	12-DEC-1997; 97US-069435P.
X				PR	17-DEC-1997; 97US-069870P.
X				PR	18-DEC-1997; 97US-068017P.
X				PR	10-MAR-1998; 98US-077450P.
X				PR	11-MAR-1998; 98US-077632P.
X				PR	11-MAR-1998; 98US-077649P.
X				PR	20-MAR-1998; 98US-078866P.
X				PR	20-MAR-1998; 98US-078939P.
X				PR	27-MAR-1998; 98US-079564P.
X				PR	27-MAR-1998; 98US-079786P.
X				PR	31-MAR-1998; 98US-080107P.
X				PR	31-MAR-1998; 98US-080194P.
X				PR	01-APR-1998; 98US-080327P.
X				PR	01-APR-1998; 98US-080333P.
X				PR	08-APR-1998; 98US-081049P.
X				PR	08-APR-1998; 98US-081070P.

[illegible]

b 741 TCACAACTGCCCCGAAACACAGGCTGCCAGCACCCCTCCCACTGCCAGACTCTGCTGCC 800
Y 904 AAGCTTGCAAGATGAGCGAAGTGAAGCAATCGATGAAGAGGACAGTGTGACGTGCTCC 963
b 801 AAGCTTGCAAGATGAGCGAAGTGAAGCAATCGATGAAGAGGACAGTGTGACGTGCTCC 960
Y 964 ATGGGGTGAGACATCTCCAGAGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGCCCG 1023
b 861 ATGGGGTGAGACATCTCCAGAGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGCCCG 920
Y 1024 GCACCCAGAGCCCCACAGCTGCTCAGCGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 1083
b 921 GCACCCAGAGCCCCACAGCTGCTCAGCGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 980
Y 1084 CCAAGGGAGCAGGAGCAGCACACTGTCAAGATGCTCTGAAGAGAGAAATGAAGAACCT 1143
b 981 CCAAGGGAGCAGGAGCAGCACACTGTCAAGATGCTCTGAAGAGAGAAATGAAGAACCT 1040
Y 1144 GTGTGATGGCGGAAAGCAGTACTCCACGCGGAGGTGTGGCACCCCGCTTCCGTGCT 1203
b 1041 GTGTGATGGCGGAAAGCAGTACTCCACGCGGAGGTGTGGCACCCCGCTTCCGTGCT 1100
Y 1204 TCGGCCCCCTGCTGCTGATCTATGCACTGTGAGGATGCCGCCAGGACTGCCAGCGTG 1263
b 1101 TCGGCCCCCTGCTGCTGATCTATGCACTGTGAGGATGCCGCCAGGACTGCCAGCGTG 1160
Y 1264 TGACCTGTCCACCGAGTACCCCTGCTGCTACCCCGAGAAAGTGGCTGGAAAGTGTGCA 1323
b 1161 TGACCTGTCCACCGAGTACCCCTGCTGCTACCCCGAGAAAGTGGCTGGAAAGTGTGCA 1220
Y 1324 AGATTGGCCAGAGGACAAAGCAGACCTGCGCCACAGTGAGATCAAGTCTTACCAAGTGT 1383
b 1221 AGATTGGCCAGAGGACAAAGCAGACCTGCGCCACAGTGAGATCAAGTCTTACCAAGTGT 1280
Y 1384 CCAAGGCCACCGGGCGGGTCTCTGCCACACATCGGTATCCCAAGGCCACAGCAACTGC 1443
b 1281 CCAAGGCCACCGGGCGGGTCTCTGCCACACATCGGTATCCCAAGGCCACAGCAACTGC 1340
Y 1444 GTCGCTTTGCTCGGACACAGGCTCGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1503
b 1341 GTCGCTTTGCTCGGACACAGGCTCGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1400
Y 1504 TAAAGATGAGGAAACTGAGGCTCAGAGGTGAAGTACTGGCCCAAGGCCACACAGCC 1563
b 1401 TAAAGATGAGGAAACTGAGGCTCAGAGGTGAAGTACTGGCCCAAGGCCACACAGCC 1460
Y 1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGTCTCCAGAAAGGCA 1623
b 1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGTCTCCAGAAAGGCA 1520
Y 1624 CAGCACTTCGACTGCTGCTGCGCCGCCACGAGGTCACCTGGAACTCTTCTAGCCAG 1683
b 1521 CAGCACTTCGACTGCTGCTGCGCCGCCACGAGGTCACCTGGAACTCTTCTAGCCAG 1580
Y 1684 ACCCTGGAGCTGAAGGTCAGGCGCTCAGCAAGAGTGAAGTCAAGCAATCAAGCACT 1743
b 1581 ACCCTGGAGCTGAAGGTCAGGCGCTCAGCAAGAGTGAAGTCAAGCAATCAAGCACT 1640
Y 1744 AACAGTTCAGATAGCTGTATTAATTTGTTTATATATATTAATTAATTAAGAGTTG 1803
b 1641 AACAGTTCAGATAGCTGTATTAATTTGTTTATATATATTAATTAATTAAGAGTTG 1700
Y 1804 CATTAACCAAAA 1817
b 1701 CATTAACCTCAAAA 1714

RESULT 20

EX78668

D ABX78668 standard; cDNA; 1732 BP.

X

C ABX78668;

X

DT 15-APR-2003 (first entry)
XX Human PRO polynucleotide #141.
DE Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
XX liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADAPT;
KW antibody-dependent enzyme mediated prodrug therapy.
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
OS
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-0176492.
XX
XX 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US21108.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21725.
PR 18-SEP-1997; 97US-05263P.
PR 18-SEP-1997; 97US-05266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
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RESULT 21

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DT 26-MAR-2003 (first entry)
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XX Human cDNA encoding secreted/transmembrane protein, PRO1557.
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XX antiarthritic; vulnary; tumour necrosis factor-alpha;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
XX
OS Homo sapiens.
XX
PN US2003022298-A1.
XX
PD 30-JAN-2003.
XX
PF 20-JUN-2002; 2002US-0176913.
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PR 05-NOV-1997; 97WO-US20069.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25106.
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PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
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PR 15-SEP-1999; 99WO-US21090.
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PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
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 DB 321 TGGGACTCGGCTCTCTGGTTCCCTCGGACTCCACGCTCGAGCCGCCACATGT 380
 QY 484 TCTGCTTTTCATGGGAGAGATCTCCCGCGGAGAGCTGGCACCCCTACTTTGGAGC 543

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741 TCACACCTGCTGCCCAACACAGTGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
904 AGCCTGCAAGATGAGGCAAGTGTGAGCAATCGATGAGAGGACAGTGTGAGTGTGCTGCTGCT 963
801 AGCCTGCAAGATGAGGCAAGTGTGAGCAATCGATGAGAGGACAGTGTGAGTGTGCTGCTGCT 860
964 ATGGGTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
861 ATGGGTGAGACATCTCTCAGGATCCATGTTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
1024 GCACCCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
921 GCACCCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
1084 CCAAGGAGCAGGACGACACACTGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
981 CCAAGGAGCAGGACGACACACTGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
1144 GTGTGATGGGGGAGAACATCTCTCCACGAGGAGGTGTGGCACCCGCTTCCGCTGCTGCTGCT 1203
1041 GTGTGATGGGGGAGAACATCTCTCCACGAGGAGGTGTGGCACCCGCTTCCGCTGCTGCTGCTGCT 1100
1204 TCGGCT 1263
1101 TCGGCT 1160
1264 TGACCTGCT 1323
1161 TGACCTGCT 1220
1324 AGATTGCT 1383
1221 AGATTGCT 1280
1384 CCAAGGACCGGGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
1281 CCAAGGACCGGGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1340
1444 GTGCT 1503
1341 GTGCT 1400
1504 TAAAGATGAGGAACCTGAGCTCAGAGAGGTGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563
1401 TAAAGATGAGGAACCTGAGCTCAGAGAGGTGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460
1564 AGAATCTTCCATTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1623
1461 AGAATCTTCCATTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCA 1520

QY 1624 CAGCACTTCCGAGCT 1683
Db 1521 CAGCACTTCCGAGCT 1580
QY 1684 ACCCTGAGCTGAGAGCT 1743
Db 1581 ACCCTGAGCTGAGAGCT 1640
QY 1744 AACAGTGGAGATGAGCT 1803
Db 1641 AACAGTGGAGATGAGCT 1700
QY 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714
RESULT 22
ABX76886
ID ABX76886 standard; cDNA; 1732 BP.
XX
AC ABX76886;
XX
DT 04-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #41.
XX
KW Human; PRO; gene; ss; tumour necrosis factor-alpha; blood; cancer;
chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;
kidney; rectum; cervix; liver; bone disorder; cartilage disorder;
XX
KW arthritis; sports injury; genetic disorder; antiarthritic; vulnery.
XX
OS Homo sapiens.
XX
XX US2003027280-A1.
XX
PD 06-FEB-2003.
XX
PF 20-JUN-2002; 2002US-0176993.
XX
XX 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21030.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04114.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06839.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.

PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 09-AUG-2001; 2001WO-US217099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063440P.
PR 28-OCT-1997; 97US-063441P.
PR 28-OCT-1997; 97US-063444P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 13-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
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PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081538P.
PR 15-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 05-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086466P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
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PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
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PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
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PR 05-JUN-1998; 98US-088654P.
PR 05-JUN-1998; 98US-088722P.
PR 05-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 10-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088876P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090576P.
PR 25-JUN-1998; 98US-090578P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 02-JUL-1998; 98US-091636P.
PR 04-AUG-1998; 98US-091606P.
PR 10-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 17-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.

Query Match	Best Local Similarity	Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Y 424	TTGGGCTGGAGCCTCCTGGGAGTAAATGAGCACTGTGCGTTTGGCAGGCCAGACATGT 483	
Y 321	TGGGACTCGCGTGTCTGGTTCCTCCCTGGACTCCCACTGGAGCCCGGCCAGACATGT 380	
Y 484	TCTGCCTTTTCCATGGGAAGAGATACTCTCCCGCGGAGAGCTGGCACTGGCACTTGGAGC 543	
Y 381	TCTGCCTTTTCCATGGGAAGAGATACTCTCCCGCGGAGAGCTGGCACTGGCACTTGGAGC 440	
Y 544	CACAAGGCTGTATGTACTGTGCTGCGTGTACTGCTCTCAGAGGGGCCCATGTGAGTGTGT 603	
Y 441	CACAAGGCTGTATGTACTGTGCTGCGTGTACTGCTCTCAGAGGGGCCCATGTGAGTGTGT 500	
Y 604	ACCGCTTCCACTGTCCGCTGTCTCACTGCGCCCTCCAGCCTGTGACGAGGACACAGCAATGCT 666	
Y 501	ACCGCTTCCACTGTCCGCTGTCTCACTGCGCCCTCCAGCCTGTGACGAGGACACAGCAATGCT 560	
Y 664	GTCCCAAGTGTGGGAACCTCACACTCCCTCTGGACTCTGGGGCCCAACCAAGTCTCGCC 723	
Y 561	GTCCCAAGTGTGGGAACCTCACACTCCCTCTGGACTCTGGGGCCCAACCAAGTCTCGCC 620	
Y 724	AGCACACGGGACACATGTATCAACACGAGAGATCTTCAGTGCCTCATGAGCTGTTCCTCT 783	
Y 621	AGCACACGGGACACATGTATCAACACGAGAGATCTTCAGTGCCTCATGAGCTGTTCCTCT 680	
Y 784	CCGCGCTGCCCCAACCAAGTGTCTCTGCACTGTCACAGGGGCCAGATCTATGCGGGCC 843	
Y 681	CCGCGCTGCCCCAACCAAGTGTCTCTGCACTGTCACAGGGGCCAGATCTATGCGGGCC 740	
Y 844	TCAACAACCTGCCCGGAACACAGGCTGCGCAGACAACCTCTCCCGTGCACAGATCTCTGTGCC 903	
Y 741	TCAACAACCTGCCCGGAACACAGGCTGCGCAGACAACCTCTCCCGTGCACAGATCTCTGTGCC 800	
Y 904	AAGCCTGTCAAAAGTAGGCGCAAGTAGCAATCGATGAAGAGGACAGTGTCACTGCTGCC 963	
Y 801	AAGCCTGTCAAAAGTAGGCGCAAGTAGCAATCGATGAAGAGGACAGTGTCACTGCTGCC 860	
Y 964	ATGGGTGAGACATCTCCAGAGTCCATGTTCAGTGTATGCTGGGAGAAAGAGAGGCCGGG 1023	
Y 861	ATGGGTGAGACATCTCCAGAGTCCATGTTCAGTGTATGCTGGGAGAAAGAGAGGCCGGG 920	
Y 1024	GCACCCCAAGCCCACTGGCTCTCAGGGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC 1083	
Y 921	GCACCCCAAGCCCACTGGCTCTCAGGGCCCTCTGAGCTTTCATCCCTCGCCACTTCAGAC 980	
Y 1084	CCAAGGGACGACGACACAACTGTCTAGATCTGCTCTGAAGAGAGAAACATTAAGAAAGCT 1143	
Y 981	CCAAGGGACGACGACACAACTGTCTAGATCTGCTCTGAAGAGAGAAACATTAAGAAAGCT 1040	
Y 1144	GTGTGCACTGGCGGAGACAGTACTTCCACGGGGAGTGTGCGACCCGGCCTTCCTGTCCT 1203	
Y 1041	GTGTGCACTGGCGGAGACAGTACTTCCACGGGGAGTGTGCGACCCGGCCTTCCTGTCCT 1100	
Y 1204	TGGGCCCTCTGCTGCATCTTATGCACTCTGTAGGATGGCCGCGCAGGAATGCGACAGGTG 1263	
Y 1101	TGGGCCCTCTGCTGCATCTTATGCACTCTGTAGGATGGCCGCGCAGGAATGCGACAGGTG 1160	
Y 1264	TGACCTGTCTCCCAACGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAGTGTCTCA 1323	
Y 1161	TGACCTGTCTCCCAACGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGGAAGTGTCTCA 1220	
Y 1324	AGATTTTGCCACAGGACAAAGACAGACCCCTGGCCACAGTGAGATCAGTCTTACCAAGTGTCT 1383	
Y 1221	AGATTTTGCCACAGGACAAAGACAGACCCCTGGCCACAGTGAGATCAGTCTTACCAAGTGTCT 1280	
Y 1384	CCAAGGACACGGGCGGGTCTCTGCTCCACACATCGGTATCTCCCAAGGCCAGACACTGCG 1443	
Y 1281	CCAAGGACACGGGCGGGTCTCTGCTCCACACATCGGTATCTCCCAAGGCCAGACACTGCG 1340	

RESULT 23	
ABX16726	
ID	ABX16726 standard; cDNA; 1732 BP.
XX	
XX	ABX16726;
XX	
XX	
XX	03-FEB-2003 (first entry)
XX	
DE	Human cDNA encoding secreted/transmembrane protein #14.

Human; ss; gene; secreted and transmembrane protein; blood;
tumour necrosis factor- α ; chondrocyte cell proliferation;
chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; bone disorder; cartilage disorder;
arthritis; sports injury.

Homo sapiens.

XX
PN US2002127584-A1.

XX
PD 12-SEP-2002.

15-JAN-2002: 2002US-0052586

XX
PR 16-SEP-1998: 98WO-US19330

PR	07-OCT-1998;	98WO-US21141
PR	01-DEC-1998;	98WO-US25108

PR 06-JAN-1999; 2000WO-US00219
PR 08-MAR-1999; 99WO-US05028

PR	14-MAY-1999;	99WO-US10733
PR	02-JUN-1999;	99WO-US12252

PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.

PR	01-DEC-1999;	99WO-US28301.
PR	02-DEC-1999;	99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414

PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601

PR 02-MAR-2000; 2000WO-US05841.

15-MAR-2000; 2000WO-US06884.
 30-MAR-2000; 2000WO-US08439.
 17-MAY-2000; 2000WO-US13705.
 22-MAY-2000; 2000WO-US14042.
 30-MAY-2000; 2000WO-US14941.
 02-JUN-2000; 2000WO-US15264.
 28-JUN-2000; 2000WO-US20710.
 08-AUG-2000; 2000WO-US23328.
 08-NOV-2000; 2000WO-US30952.
 01-DEC-2000; 2000WO-US32678.
 20-DEC-2000; 2000WO-US34956.
 28-FEB-2001; 2001WO-US06520.
 01-JUN-2001; 2001WO-US17800.
 20-JUN-2001; 2001WO-US19692.
 29-JUN-2001; 2001WO-US21066.
 09-JUL-2001; 2001WO-US21735.
 29-AUG-2001; 2001WO-US27099.
 18-SEP-1997; 97US-059263P.
 18-SEP-1997; 97US-059266P.
 17-OCT-1997; 97US-062250P.
 21-OCT-1997; 97US-063486P.
 24-OCT-1997; 97US-063120P.
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 31-OCT-1997; 97US-064103P.
 13-NOV-1997; 97US-064311P.
 21-NOV-1997; 97US-066120P.
 24-NOV-1997; 97US-066466P.
 24-NOV-1997; 97US-066772P.
 11-DEC-1997; 97US-069335P.
 12-DEC-1997; 97US-069425P.
 17-DEC-1997; 97US-069870P.
 18-DEC-1997; 97US-068017P.
 10-MAR-1998; 98US-077450P.
 11-MAR-1998; 98US-077632P.
 11-MAR-1998; 98US-077649P.
 20-MAR-1998; 98US-078886P.
 20-MAR-1998; 98US-078939P.
 27-MAR-1998; 98US-079664P.
 27-MAR-1998; 98US-079786P.
 31-MAR-1998; 98US-080107P.
 31-MAR-1998; 98US-080194P.
 01-APR-1998; 98US-080327P.
 01-APR-1998; 98US-080333P.
 08-APR-1998; 98US-081049P.
 08-APR-1998; 98US-081070P.
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 15-APR-1998; 98US-081838P.
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 21-APR-1998; 98US-082569P.
 22-APR-1998; 98US-082704P.
 22-APR-1998; 98US-082757P.
 28-APR-1998; 98US-083322P.
 29-APR-1998; 98US-083495P.
 29-APR-1998; 98US-083496P.
 29-APR-1998; 98US-083499P.
 05-MAY-1998; 98US-083559P.
 05-MAY-1998; 98US-084366P.
 06-MAY-1998; 98US-084414P.
 07-MAY-1998; 98US-084639P.
 07-MAY-1998; 98US-084640P.
 07-MAY-1998; 98US-084643P.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI: 2003-066893/06.
 DR P-PSDB; ABU10650.
 XX Novel isolated PRO polypeptides e.g., PRO1079, PRO827, PRO791, PRO1131,
 PT PRO316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333, useful for
 PT stimulating release of tumor necrosis factor-alpha from human blood -
 XX
 PS Claim 2; Fig 281; 701pp; English.
 XX
 XX The invention relates to an isolated PRO polypeptide comprising at least
 CC 80% sequence identity to the protein sequences appearing as ABU10510-
 CC ABU10814 (including a version lacking its associated signal peptide, or
 CC an isolated extracellular domain of a PRO polypeptide with or without
 CC its associated signal peptide. Also included are the nucleic acids
 CC encoding the PRO proteins (being secreted and transmembrane proteins)
 CC appearing as ABX15886-ABX16590, PRO expression vectors, host cells,
 CC chimeric PRO fusion proteins, an anti-PRO antibody and a PRO
 CC derived oligonucleotide sequence. The PRO polypeptides are useful for
 CC stimulating release of tumor necrosis factor-alpha from human blood.
 CC The PRO polypeptide PRO6029 is useful for stimulating proliferation or
 CC differentiation of chondrocyte cells. The PRO polypeptides as specified
 CC in the specification and having differential expression in tumour cells,
 CC are useful for detecting presence of tumour in a mammal (such as adrenal
 CC tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal
 CC tumour, cervical tumour or liver tumour. The PRO polypeptide PRO6029 is
 CC useful for treating various bone and/or cartilage disorders such as
 CC arthritis, and sports injuries. The PRO polypeptides are useful for
 CC screening compounds to identify ant/agonists. PRO nucleic acids
 CC are useful as hybridisation probes, in chromosome and gene mapping,
 CC in the generation of anti-sense RNA and DNA, for the preparation of PRO
 CC polypeptides and for generating knock-out animals. The present
 CC sequence encodes a PRO polypeptide.
 XX Sequence 1732 BP; 369 A, 592 C; 425 G; 346 T; 0 other;
 XX

Query Match 73.9%; Score 1342.8; DB 25; Length 1732;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCCTCTCGGACTAAATGGGCTGCTGGTTTCCAGGCCACACATGT 483
 Db 321 TGGGACTCGCGCTGCTCTGGTTCCCTCGGATCCCGCTCGAGCGCCCGCCGACATGT 380
 QY 484 TCTGCTTTTCCATGGGAAGAGATATCTCCCGCGGAGAGCTGGACCCCTACTTGGAC 543
 Db 381 TCTGCTTTTCCATGGGAAGAGATATCTCCCGCGGAGAGCTGGACCCCTACTTGGAC 440
 QY 544 CACAGGCTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
 Db 441 CACAGGCTGATGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
 QY 604 ACCGCTCCACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
 Db 501 ACCGCTCCACTGTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
 QY 664 GTCCCAAGTGTGGAACTCCTACACTCCCTCTGGAATCCCGGCCCAACAAAGTCTGCC 723
 Db 561 GTCCCAAGTGTGGAACTCCTACACTCCCTCTGGAATCCCGGCCCAACAAAGTCTGCC 620
 QY 724 AGCACAGGACCATGTAACACACGAGAGATCTTCAAGTCCCATGAGCTGTTCCCT 783
 Db 621 AGCACAGGACCATGTAACACACGAGAGATCTTCAAGTCCCATGAGCTGTTCCCT 680
 QY 784 CCGGCTGCCCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
 Db 681 CCGGCTGCCCAACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
 QY 844 TCACAACTGCCCCGAAACCAAGGTGCCAGCAACCCCTCCCGCTGCCAGCTCTGCTGCTGCC 903
 Db 741 TCACAACTGCCCCGAAACCAAGGTGCCAGCAACCCCTCCCGCTGCCAGCTCTGCTGCTGCC 800
 QY 904 AAGCTGCAAGATGAGCAAGTGAATCGATGAAGAGGACAGTGTGACGTGCTGCC 963

.

KW	Human; ss; gene; chordin homologue; LP236; neurological disorder;
KW	Alzheimer's disease parkinson's disease; wound; tissue repair;
KW	bone fracture; spinal cord injury; pressure ulcer; diabetic ulcer;
KW	venous stasis ulcer; burn; cardiovascular disorder; atherosclerosis;
KW	thrombosis; heart failure; proliferative disorder; osteosarcoma;
KW	breast cancer; leukaemia; prostate cancer; bone mineral density disorder;
KW	osteopaenia-related disorder; fibrotic disorder; cirrhosis;
KW	chronic asbestosis; restenosis; Gaucher's disease; Marfan's disease;
KW	anaemia; diabetes mellitus; osteoporosis; transgenic.
XX	Homo sapiens.
OS	
XX	
XX	Key Location/Qualifiers
FT	misc_feature 307..1660
FT	/*tag= a
FT	/note="This region is specifically claimed in claim 2"
FT	CDS 307..1662
FT	/*tag= b
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FT	sig_peptide 307..387
FT	/*tag= c
FT	misc_feature 387..1660
FT	/*tag= d
FT	/note="This region is specifically claimed in claim 2"
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FT	/*tag= e
FT	/label= Mature_LP233
XX	
XX	WO200208277-A2.
PX	
PN	
PD	31-JAN-2002.
PI	
PP	05-JUL-2001; 2001WO-US16517.
PR	
PR	19-JUL-2000; 2000US-219359P.
PR	04-MAY-2001; 2001US-288892P.
PA	(EILIL) LILLY & CO ELI.
XX	
PI	Alvarez E, McEntire JK, Smith RC, Su EW;
PI	WPI; 2002-280599/32.
DR	P-PSDB; AAU78174.
PT	
PT	Novel isolated LP polypeptide having significant sequence similarity to
PT	cysteine-rich regions of chordin, useful for treating neurological,
PT	cardiovascular, proliferative fibrotic and osteopaenia-related disorders
PT	_
XX	
XX	Claim 3; Page 15-18; 149pp; English.
XX	
CC	The invention relates to isolated LP polypeptides (which have
CC	significant sequence similarity to the cysteine-rich regions of chordin
CC	being LP226, LP233 and LP236) and encoding polynucleotides. The
CC	mature portions of the LP proteins and the region of the nucleic acid
CC	encoding them are also included. Also included are a vector
CC	comprising the polynucleotide, a host cell comprising the vector, an
CC	anti-LP antibody and ant/agonists of the LP proteins. LP is useful in the
CC	manufacture of a medicament. LP, LP polynucleotide Agonists or
CC	antagonists of LP are useful for diagnosis and treatment of a
CC	neurological disorder (e.g. Alzheimer's disease and
CC	Parkinson's disease), a disorder requiring wound or tissue repair (where
CC	the disorder is selected from bone fracture, spinal cord injury, pressure
CC	ulcer, diabetic ulcer, venous stasis ulcer, and burn) a cardiovascular
CC	disorder (e.g. atherosclerosis, thrombosis and heart failure), a
CC	proliferative disorder such as osteosarcoma, breast cancer, leukaemia
CC	and prostate cancer, a disorder associated with loss of bone mineral
CC	density, an osteopaenia-related disorder, or a fibrotic disorder
CC	(e.g. cirrhosis and chronic asbestosis), restenosis, Gaucher's disease,
CC	Marfan's disease, anaemia, diabetes mellitus, osteoporosis and many other
CC	diseases and disorders listed in the specification. LP is useful for
CC	identifying compounds that bind to LP, and to isolate correlative
CC	ligands. LP polynucleotide as hybridisation probes, in chromosome and

[illegible]

P-PSDB; AAB68077.
Nucleic acids encoding splice variants of a chordin like homolog, useful in the treatment of bone injuries, diseases involving with the female reproductive tract, diseases involving sexual hormone abnormalities and cardiovascular disorders.
Claim 1; Page 180-181; 203pp; English.
The present sequence encodes a splice variant of a chordin like homologue (CLH). The protein is a homologue to the known chordin like the von-Willebrand factor type C (WFPC) domain repeat, which is found 2-4 times in these multi-domain proteins. The present protein contains 3 WFPC repeats. CLH proteins and polynucleotides can be used for the treatment of diseases which can be ameliorated, cured or prevented by raising the level of a CLH. The nucleic acids, expression vectors, proteins and antibodies are useful in the treatment of a disease selected from diseases manifested in non-normal bone formation and non-normal bone modelling, bone injuries, diseases involved with the female reproductive tract, diseases of disorders involved with abnormal sexual differentiation, recurrent miscarriages, tumours of the uterus, breast or prostate, diseases involving sexual hormone abnormalities, cardiovascular disorders, neuronal diseases of the CNS (central nervous system), or neurodegenerative diseases and diseases involving non-normal developments of neurons.
Sequence 1722 BP; 351 A; 594 C; 425 G; 352 T; 0 other;
Query Match 73.6%; Score 1338; DB 22; Length 1722;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
424 TTGGCTGGAGCCTCTGGGACTAATGACATGCTGTCGTTGGCCAGGCCACACATGT 483
329 TGGGACTCGGCTGTCTGGTTCCTCCCTGAGCTCCACGCTCCAGCCGCCACACATGT 388
484 TCTGCTTTTCCATGGGAAGAGATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC 543
389 TCTGCTTTTCCATGGGAAGAGATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC 448
544 CACAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
449 CACAGGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508
504 ACCGCTCCACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
509 ACCGCTCCACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
664 GTCCCAAGTGTGGAACTCACTCCCTCTGGACTCCGGGCCCCCAACAAAGTCTGCTGCC 723
569 GTCCCAAGTGTGGAACTCACTCCCTCTGGACTCCGGGCCCCCAACAAAGTCTGCTGCC 628
724 AGCAACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 783
629 AGCAACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 688
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689 CCGCTCTGCCCAACACGATGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
844 TCAACATGCTGCCCAACACGATGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
749 TCAACATGCTGCCCAACACGATGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
904 AGCCTGTCAAGATGAGGCAAGTGGACATCGGATGAAGAGGACAGTGTGTCAGTCTGCTCC 963
809 AGGCTGTCAAGATGAGGCAAGTGGACATCGGATGAAGAGGACAGTGTGTCAGTCTGCTCC 868
964 ATGGGTGAGACATCTCAGATCCATGTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
869 ATGGGTGAGACATCTCAGATCCATGTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 928
1024 GCACCCCGACCCCACTGGGCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTTTCAGAC 1083

929 GCACCCCGACCCCACTGGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTCATAC 988
1084 CCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1143
989 CCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1048
1144 GTGTGATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1203
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1109 TCGGCCCCCTTGGCCCTGATCCTATGACCTGTGAGGATGGCCGCGAGGAGTCCAGGAGGTG 1168
1264 TGACCTGTCCCAACGAGTACCCCTGCGCTCCACCGGAGGAGTGGTGGGAGGAGTCTGCA 1323
1169 TGACCTGTCCCAACGAGTACCCCTGCGCTCCACCGGAGGAGTGGTGGGAGGAGTCTGCA 1228
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1229 AGATTTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1288
1384 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1443
1289 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348
1444 GTGCTTTTGGCCCTGGGACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1503
1349 GTGCTTTTGGCCCTGGGACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1408
1504 TAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1563
1409 TAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1468
1564 AGAATCTTCCACTTGACTCAGATCAAGAAGTCAAGAAGTCAAGAAGTCAAGAAGTCAAGA 1623
1469 AGAATCTTCCACTTGACTCAGATCAAGAAGTCAAGAAGTCAAGAAGTCAAGAAGTCAAGA 1528
1624 CAGCACTTCCCACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683
1529 CAGCACTTCCCACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1588
1684 ACCCTGGAGCTGAGGAGTCAAGGCTGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 1743
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1744 AACAGTTGAGATGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGT 1803
1649 AACAGTTGAGATGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGT 1708
1804 CATAACCATCAAAA 1817
1709 CATAACCATCAAAA 1722
RESULT 26
AAF84771
ID AAF84771 standard; DNA; 1722 BP.
XX AC AAF84771;
XX DT 09-JUL-2001 (first entry)
XX DE Nucleotide sequence of a human chordin-like homologue splice variant.
XX KW Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
XX KW von-Willebrand factor type C repeat; WFPC repeat; bone formation;
XX KW reproductive disease; sexual differentiation; miscarriage; tumour;
XX KW sexual hormone; cardiovascular disorder; neuronal disease;
XX KW neurodegenerative disease; neuron development; ss.
OS Homo sapiens.

Query Match	71.4%;	Score 1297;	DB 22;	Length 1567;
Best Local Similarity	86.2%;	Pred. No. 0;		

2Y	770	TGAGCTGTTTCCCTCCCGCTGCCCAA--CAGATGTGTCTCTGCAAGCTGACAGAGGGCC	828
3B	436	TGAGCTGTATCCCTTCCCGCTTCCGCAACCACTGTGCTCTGCAAGCTGCA	495
2Y	829	AGATCTACTTGGGGCTCACAACTTCCCGCAACAGAGCTGCCAGCA	888
3B	496	AGATCTACTTGGGGCTCACAACTTCCCGCAACAGAGCTGCCAGCA	555
2Y	989	CAGACTCTCTGTCGCAAGCTGCAAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGACA	948
3B	556	CAGACTCTCTGTCGCAAGCTGCAAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGACA	615
2Y	949	GTGTGCAAGCTGCTCAATGGGGTGAAGACATCTCAGGATCCATGTTCCAGTGAATCTGGGA	1008
3B	616	GTGTGCAAGCTGCTCAATGGGGTGAAGACATCTCAGGATCCATGTTCCAGTGAATCTGGGA	675
2Y	1009	GAAGAAGAGGCGCGGCAACCCAGACCCCACTGGGCTTACGCGCCCTCTGAGCTTCAATCC	1068
3B	676	GAAGAAGAGGCGCGGCAACCCAGACCCCACTGGGCTTACGCGCCCTCTGAGCTTCAATCC	735
2Y	1069	CTCGCCCACTTCAGACCCCAAGGGAGCAGGACAGCAAACTGTCAAGATCGTCTGAAGGAGA	1128
3B	736	CTCGCCCACTTCAGACCCCAAGGGAGCAGGACAGCAAACTGTCAAGATCGTCTGAAGGAGA	795
2Y	1129	AACTAAGAAAGCCCTGTGTGCAATGGGCGGAGACGTACTCTCCACGGGAGAGTGTGGCACC	1188
3B	796	AACTAAGAAAGCCCTGTGTGCAATGGGCGGAGACGTACTCTCCACGGGAGAGTGTGGCACC	855
2Y	1189	CGGCTTTCGTCGCTTGGCCCTTGGCCCTGCACTCTATGCACTCTGAGAGATGCGCCGCC	1248
3B	856	CGGCTTTCGTCGCTTGGCCCTTGGCCCTGCACTCTATGCACTCTGAGAGATGCGCCGCC	915
2Y	1249	AGGACTGCGAGAGTGTGACCTGCTCCCACTCGATACC-----CTGCGCTCACCCCGAGAA	1303
3B	916	AGGACTGCGAGAGTGTGACCTGCTCCCACTCGATACC-----CTGCGCTCACCCCGAGAAA	975
2Y	1304	AGTGGCTGGGAAGTCTCTCAAGATTTGCCCCAGGAGCAAAAGCAGACCTTGGGCACTGTGA	1363
3B	976	GTGGCTTGGGAAGTCTCTCAAGATTTGCCCCAGGAGCAAAAGCAGACCTTGGGCACTGTGA	1035
2Y	1364	GATCAGTTCTTACCAAGTGTCCCAAGGCAACGGGCGCGGTCTCTGCTCCACACATCGGTATC	1423
3B	1036	GATCAGTTCTTACCAAGTGTCCCAAGGCAACGGGCGCGGTCTCTGCTCCACACATCGGTATC	1095
2Y	1424	CCGAAGCCACAGACACTTGGCTTGGCTTGGCCCTTGGCAACAGAGGCTCTCGAGCTTGGTGGGA	1483
3B	1096	CCGAAGCCACAGACACTTGGCTTGGCTTGGCCCTTGGCAACAGAGGCTCTCGAGCTTGGTGGGA	1155
2Y	1484	GATCTACTCTCTGAGCTTGGTAAAGATGAGGAAAC--TGAGGCTCA--GAGAGGTCAAGTA	1541
3B	1156	GATCTACTCTCTGAGCTTGGTAAAGATGAGGAAACCTTGAGGCTCTGAGAGAGGTGAAGTA	1215
2Y	1542	CTTGCGCCCAAGGGCCACACAGCCAGAAATCTTCCACTTGAATCAGATCAAGAAAGTCAGGAA	1601
3B	1216	CTTGCGCCCAAGGGCCACACAGCCAGAAATCTTCCACTTGAATCAGAAAGATCAGGAA	1275
2Y	1602	GCAAGACTT--CCAGAAGAAGGCAACAGACATTCCTCGACTGCTCGCTGGCCCCCAACGAGTTC	1660
3B	1276	GCAAGACTTCCAGAAAGAGGCAACAGCACTTCCGACTGCTGCTGGCCCCCAACGAGTTC	1335
2Y	1661	ACTTGGAGACGCTTCTTAGCCACAGACCTCTGAGCTGAAGGTCAACGCCAGTCCAGACAAG	1720
3B	1336	ACTTGGAGACGCTTCTTAGCCACAGACCTCTGAGCTGAAGGTCAACGCCAGTCCAGACAAG	1395
2Y	1721	TGACCAAGACATTAACAAAGACCTTACAGTGTGCGAGATGAGAGCTGTATAATTTGTTGTTAT	1780
3B	1396	TGACCAAGACATTAACAAAGACCTTACAGTGTGCGAGATGAGAGCTGTATAATTTGTTGTTAT	1455
2Y	1781	ATATATTATTAATAAGAGAGTGGCATTAACCATCAAAA	1817
3B	1456	ATATATTATTAATAAGAGAGTGGCATTAACCATCAAAA	1492

XX	RESULT 30
XX	AAF84770
II	AAF84770 standard; DNA; 1281 BP.
XX	AAF84770;
XX	AAF84770;
DT	09-JUL-2001 (first entry)
DE	Nucleotide sequence of a human chordin-like homologue.
XX	Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
XX	von-Willebrand factor type C repeat; VWF repeat; bone formation;
KW	reproductive disease; sexual differentiation; miscarriage; tumour;
KW	sexual hormone; cardiovascular disorder; neuronal disease;
KW	neurodegenerative disease; neuron development; ss.
XX	Homo sapiens.
OS	
XX	
FF	Key Location/Qualifiers
XX	2..1198
CDS	
FT	/*tag= a
FT	/trans_except= "(pos: 599..601, aa: Xaa) "
FT	/product= "chordin-like homologue"
FT	/note= "Xaa represents an unspecified amino acid"
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PN	WO200134796-A1.
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XX	
ED	17-MAY-2001.
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FF	10-NOV-2000; 2000WO-IL00736.
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XX	
PR	10-NOV-1999; 99IL-0132846.
PR	28-DEC-1999; 99IL-0133767.
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PA	{COMP-} COMPUGEN LTD.
XX	
PI	Toporok A, Biton S, Savitzky K, Bernstein J;
DR	WPI; 2001-308783/32.
DR	P-PSDB; AAB68073.
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XX	
PT	Nucleic acids encoding splice variants of a chordin like homology.
PT	useful in the treatment of bone injuries, diseases involved with the
PT	fetal reproductive tract, diseases involving sexual hormone
PT	abnormalities and cardiovascular disorders -
XX	
XX	
PS	Claim 1; Page 178; 203pp; English.
XX	
CC	The present sequence encodes a chordin like homologue (CLH). The protein
CC	is a homologue to the known chordins within the von-Willebrand factor
CC	type C (VWF) domain repeat, which is found 2-4 times in these
CC	multi-domain proteins. CLH proteins and polynucleotides can be used for
CC	the treatment of diseases which can be ameliorated, cured or prevented by
CC	raising the level of a CLH. The nucleic acids, expression vectors,
CC	proteins and antibodies are useful in the treatment of a disease selected
CC	from diseases manifested in non-normal bone formation and non-normal bone
CC	modelling, bone injuries, diseases involved with the female reproductive
CC	tract, diseases of disorders involved with abnormal sexual
CC	differentiation, recurrent miscarriages, tumours of the uterus, breast
CC	or prostate, diseases involving sexual hormone abnormalities,
CC	cardiovascular disorders, neuronal diseases of the CNS (central nervous
CC	system), or neurodegenerative diseases and diseases involving non-normal
CC	developments of neurons.
XX	
SO	Sequence 1281 BP; 313 A; 405 C; 335 G; 227 T; 1 other;

Query Match 59.1%; Score 1256.4; DB 22; Length 1281;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1271; Conservative 0; Mismatches 7; Indels 1; Gaps 1.

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64	TTGTTTACCGGCTTCACATGTTCGGCTCGTTCACATGCGCCCGAGCTGTGTACGGAGGCCACAGCA	123
659	ATGCTGTCCAAAGTGTGTGGAACTTCACATCTCCCTGTGGACCTCCGGGCCCCACCAAAGTC	718
124	ATGCTGTCCAAAGTGTGTGGAACTTCACATCTCCCTGTGGACCTCCGGGCCCCACCAAAGTC	183
719	CTGCCAGCAAAACGGGACCAATGACAAACAGAGAGATCTTCAGTGCCTCATGAGCTGT	778
184	CTGCCAGCAAAACGGGACCAATGACAAACAGAGAGATCTTCAGTGCCTCATGAGCTGT	243
779	CCCTCTCCCGCTGCCCAACAGAGTGTCTCTCTGACGCTGACAGAGGGCCAGATCTTACTG	838
244	CCCTCTCCCGCTGCCCAACAGAGTGTCTCTCTGACGCTGACAGAGGGCCAGATCTTACTG	303
839	CGGCTTCACAACTGCCCCCGAAACAGAGCTGCCAGACCCCTCCCGCTGCGACATCTCTG	898
304	CGGCTTCACAACTGCCCCCGAAACAGAGCTGCCAGACCCCTCCCGCTGCGACATCTCTG	363
899	CTGCCAAGCTCCAAAGATGAGCAAGTAGAGCAATCGGATGAAGAGGACAGTCTGCAGTC	958
364	CTGCCAAGCTCCAAAGATGAGCAAGTAGAGCAATCGGATGAAGAGGACAGTCTGCAGTC	423
959	GCTCCATGAGGCTGAGACATCTCTCAGAGTCCATGTTCCATGTGCTCGGAGAAAGAGG	1018
424	GCTCCATGAGGCTGAGACATCTCTCAGAGTCCATGTTCCATGTGCTCGGAGAAAGAGG	483
1019	CCGGGGACCCGAGCCCCACTGCGCTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTT	1078
484	CCGGGGACCCGAGCCCCACTGCGCTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTT	543
1079	CAGACCCAAAGGAGCAGGCAAGCACAATGTCAAATCTGCTTGAAGAGAGAAAACATAGAA	1138
544	CAGACCCAAAGGAGCAGGCAAGCACAATGTCAAATCTGCTTGAAGAGAGAAAACATAGAA	603
1139	AGCTGTGTGCATGCGGGGAAGACGTACTCCACAGGGGAGGTGTGGCACCCGCGCTTCG	1198
604	AGCTGTGTGCATGCGGGGAAGACGTACTCCACAGGGGAGGTGTGGCACCCGCGCTTCG	663
1199	TGCTTCGCGCCCTTGTCCCTGCTCACTCTATGCACTGTGAGGATGCGCGCAGGACTGCCA	1258
664	TGCTTCGCGCCCTTGTCCCTGCTCACTCTATGCACTGTGAGGATGCGCGCAGGACTGCCA	723
1259	CGTGTGTGACCTGTTCCTCCACGAGTACCCCTGCGCTCACCCCGAGAAAGTGCTGGGAGTG	1318
724	CGTGTGTGACCTGTTCCTCCACGAGTACCCCTGCGCTCACCCCGAGAAAGTGCTGGGAGTG	783
1319	CTGCAGATTTGCCACAGAGACAAGACAGACCTCTGCGCAGTGAGATCAAGTTCTACCA	1378
784	CTGCAGATTTGCCACAGAGACAAGACAGACCTCTGCGCAGTGAGATCAAGTTCTACCA	843
1379	GTGTCCCAAGGACACCGCGCGGGTCTCTGTCCAACATCGGTATCCCAAGCCGACAA	1438
844	GTGTCCCAAGGACACCGCGCGGGTCTCTGTCCAACATCGGTATCCCAAGCCGACAA	903
1439	CTGCGTCTGCTTTGCCCTGTGGAAACAGAGGCTCTGGAATCTTACCTCTGGAA	1498
904	CTGCGTCTGCTTTGCCCTGTGGAAACAGAGGCTCTGGAATCTTACCTCTGGAA	963
1499	GCTGGTAAAGATGAGGAAACTCAGGCTCAAGAGGTTGAAGTACTCGGCCCAAGGCCACA	1558
964	GCTGGTAAAGATGAGGAAACTCAGGCTCAAGAGGTTGAAGTACTCGGCCCAAGGCCACA	1023
1559	CAGCCAGAACTCTTCCAATTGACTCAGATCAAGAAAGTTCAGGAAACAAGATCTTCAGAA	1618
1024	CAGCCAGAACTCTTCCAATTGACTCAGATCAAGAAAGTTCAGGAAACAAGATCTTCAGAA	1082
1619	AGGCAACAGACTTCCGACTGCTCGTGGCGCCCAAGAGTCACTTGGAACTCTTCCTAG	1678
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Qy	1679	CCGAGACCCCTGGAGCTGCAAGGTCAGCCGCGCTCCAGACAAAGTGCACCAAGACATTAACAAA	1739
Db	1143	CCGAGACCCCTGGAGCTGCAAGGTCAGCCGCGCTCCAGACAAAGTGCACCAAGACATTAACAAA	1202
Qy	1739	GACCTAACAGTTGCAGATATGAGCTGTATAAATTGTTGTTATTAATATTAATAATAAGA	1798
Db	1203	GACCTAACAGTTGCAGATATGAGCTGTATAAATTGTTGTTATTAATATTAATAATAAGA	1262
Qy	1799	AGTTGCATTAACCATCAAAA	1817
Db	1263	AGTTGCATTAACCATCAAAA	1281
RESULT 31			
ABKL124			
ID	ABKL12124	standard; cDNA; 1406 BP.	
AC	XX		
CC	ABKL12124;		
DT	05-JUN-2002	(first entry)	
DE	Human cDNA encoding chordin homologue LP226.		
XX	Human; ss; gene; chordin homologue; LP226; neurological disorder;		
KW	Alzheimer's disease Parkinson's disease; wound; tissue repair;		
KW	bone fracture; spinal cord injury; pressure ulcer; diabetic ulcer;		
KW	venous stasis ulcer; burn; cardiovascular disorder; atherosclerosis;		
KW	thrombosis; heart failure; proliferative disorder; osteosarcoma;		
KW	breast cancer; leukaemia; prostate cancer; bone mineral density disorder;		
KW	osteopenia-related disorder; fibrotic disorder; cirrhosis;		
KW	chronic asbestosis; restenosis; Gaucher's disease; Marfan's disease;		
KW	anemia; diabetes mellitus; osteoporosis; transgenic.		
XX	Hom sapiens.		
Key	Location/Qualifiers		
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FT		/tag= a	
FT		/note= "This region is specifically claimed in claim 2"	
FT	CDS	29..1317	
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FT		/product= "LP226"	
FT	sig_peptide	29..109	
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FT		/label= Mature_LP226	
XX	WO200208277-A2.		
PN			
PD	31-JAN-2002.		
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PF	05-JUL-2001; 2001WO-US16517.		
PP			
PR	19-JUL-2000; 2000US-219359P.		
PR	04-MAY-2001; 2001US-288892P.		
XX			
PA	(ELIL) LILLY & CO ELI.		
PI	Alvarez E, McEntire JK, Smith RC, Su EW;		
DR	WPI; 2002-280599/32.		
DR	P-PSDB; AAU78172.		
XX			
PT	Novel isolated LP polypeptide having significant sequence similarity to		
PT	cysteine-rich regions of chordin, useful for treating neurological,		
PT	cardiovascular, proliferative fibrotic and osteopenia-related disorders		
PT			

MDX

Human; chordin-like-2 protein; CHL-2; hypotensive; cardiac; cytostatic; rheumatoid arthritis; cachexia; arrhythmia; osteopetrosis; hepatitis; hypertension; myocardial infarction; stomach cancer; ulcer; gene therapy;

KW hypertension; myocardial infarction; stomach cancer; ulcer; gene therapy;
KW hypertension; myocardial infarction; stomach cancer; ulcer; gene therapy;

604	ACGGCTCCACTGTCGCTCTGTCACATCGCCCCCAAGCCTGTGA	CGGAGCCACACAGCAATGCT	663
398	ACGGCTCCACTGTCGCTCTGTCACATCGCCCCCAAGCCTGTGA	CGGAGCCACACAGCAATGCT	457
664	GTCCAAAGTGTGTGGAACCTCAACATCCCTCTGGA	CTCCGGGCCCAACAAAGTCTCTGCC	723
458	GTCCAAAGTGTGTGGAACCTCAACATCCCTCTGGA	CTCCGGGCCCAACAAAGTCTCTGCC	517
724	AGCAACAACGGGACCATGTACCAACACGGAGAGATCTT	CAGTGCCTCCATGAGCTGTCTCCCT	783
518	AGCAACAACGGGACCATGTACCAACACGGAGAGATCTT	CAGTGCCTCCATGAGCTGTCTCCCT	577
784	CCGGCTCCGCCAAACAAGTGTCTCTGCAAGTGCACAGAGG	GCCAGATCTACTGCGGCC	843
578	CCGGCTCCGCCAAACAAGTGTCTCTGCAAGTGCACAGAGG	GCCAGATCTACTGCGGCC	637
844	TCACAACCTGCCCCCGAACAGGCTGCCAGCACCCCTCC	CGCTGCCAGACTCCTGCTGCC	903
638	TCACAACCTGCCCCCGAACAGGCTGCCAGCACCCCTCC	CGCTGCCAGACTCCTGCTGCC	697
904	AAGCTCTGCAAGAATGAGGCAAGTGAAGCAATCGATGA	AGAGGACAGTGTGCAAGTCTGCTCC	963
698	AAGCTCTGCAAGAATGAGGCAAGTGAAGCAATCGATGA	AGAGGACAGTGTGCAAGTCTGCTCC	757
964	ATGGGGTGGACATCCCTCAGGATCCATGTCCTCAGTGA	TCCTGGGAAAGAGAGGCCCGG	1023
758	ATGGGGTGGACATCCCTCAGGATCCATGTCCTCAGTGA	TCCTGGGAAAGAGAGGCCCGG	817
1024	GCACCGAGCCCGCATGCGCTCAGGGCCCTGAGCTTCAT	CCCTGCCACTCTCAGAC	1083
818	GCACCGAGCCCGCATGCGCTCAGGGCCCTGAGCTTCAT	CCCTGCCACTCTCAGAC	877
1084	CCAGGGAGCAGGACGACAACTGTCAAGATGCTCTGA	AGGAGAAACATAGAAGGCT	1143
878	CCAGGGAGCAGGACGACAACTGTCAAGATGCTCTGA	AGGAGAAACATAGAAGGCT	937
1144	GTGTGCATGCGGGAGACGTACTCCACGGGAGGTGTGG	CACCGGCCCTTCGTGCT	1203
938	GTGTGCATGCGGGAGACGTACTCCACGGGAGGTGTGG	CACCGGCCCTTCGTGCT	997
1204	TCGGCCCTTTGCCCTGCATCCTTACACTGTGAGGATG	CGCCACGAGCTGCCAGCGTG	1263
998	TCGGCCCTTTGCCCTGCATCCTTACACTGTGAGGATG	CGCCACGAGCTGCCAGCGTG	1057
1264	TGACCTGTCCCAACAGTACCCCTGCGCTCACCCCGA	AGAGTGGCTGGGAAGTCTGCA	1323
1058	TGACCTGTCCCAACAGTACCCCTGCGCTCACCCCGA	AGAGTGGCTGGGAAGTCTGCA	1117
1324	AGATTTCGCCAGAGGACAGAGCAGACCTGTGCCAC	ACTGAGATCAAGTCTACCAAGTCTC	1383
1118	AGATTTCGCCAGAGGACAGAGCAGACCTGTGCCAC	ACTGAGATCAAGTCTACCAAGTCTC	1177
1384	ACAGGACACGGGCGGGTCTCGTCCACATCGGTATCC	CCAGACCCCGACACACTGC	1443
1178	ACAGGACACGGGCGGGTCTCGTCCACATCGGTATCC	CCAGACCCCGACACACTGC	1237
1444	GTTCCTTTGCCCTTGGAAACACAGAGGCTCGGACTT	GTGTGGAGATCTACTCTGGAAGCTGG	1503
1238	GTTCCTTTGCCCTTGGAAACACAGAGGCTCGGACTT	GTGTGGAGATCTACTCTGGAAGCTGG	1297
1504	TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGT	ATCTTGCCCAAGGCCACACAGCC	1563
1298	TGAAG-----	-----	1303
1564	AGATPTCTTCACTTGACTCAGATCAAGAAATCAG	GAAGCAAGATCTCAGAAAGGCA	1623
1304	-GAATPTCTTCACTTGACTCAGATCAAGAAATCAG	GAAGCAAGATCTCAGAAAGGCA	1362
1624	CAGCACTTCCGACTGTCTCGTGGCCCCCAAGAGG	TCACTGGAAAGTCTTCTCTAGGCCAG	1683
1363	CAGCACTTCCGACTGTCTCGTGGCCCCCAAGAGG	TCACTGGAAAGTCTTCTCTAGGCCAG	1422

1684 ACCCTGGAGCTGAAGGTCAACGCCGAGTCFCAGCAAAAGTGACCAAGACATACCAAGACCT 1743
1423 ACCCTGGAGCTGAAGGTCAACGCCGAGTCFCAGCAAAAGTGACCAAGACATACCAAGACCT 1482
1744 AACAGTTGCGAGATATGAGCTGTATAATGTGTGTTATATATAATAATAATAAGAGTTG 1803
1483 AACAGTTGCGAGATATGAGCTGTATAATGTGTGTTATATATAATAATAATAAGAGTTG 1542
1804 CATAACCATCAAAA 1817
1543 CATTACCCCTCAAAA 1556

RESULT 33
US03537
AA03537 standard; cDNA; 1290 BP.
AA03537;
29-AUG-2001 (first entry)
cDNA encoding Novel Human Protein, NHP #2.
Human; Novel Human Protein; NHP; diagnostic; drug screening; cancer;
clinical trial monitoring; physiological disorder; behavioural disorder;
infectious disease; gene therapy; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 1..1290
/*tag= a
/product= "Novel human protein, NHP #2"
WO200129084-A2.
26-APR-2001.
18-OCT-2000; 2000WO-US28803.
18-OCT-1999; 99US-0160106.
29-OCT-1999; 99US-0162547.
(LEXI-) LEXICON GENETICS INC.
Turner CA, Donoho G, Nehls M, Hilbun E, Zambrowicz B, Sands AT;
WPI: 2001-290898/30.
P-FSDS; AAU02750.
X Nucleic acids encoding novel human proteins (NHP), useful for treating
X physiological or behavioural disorders, cancers and infectious diseases
X .
X Disclosure; Page 60; 63pp; English.
X
X The sequence represents the coding sequence of novel human protein,
X NHP #2, isolated from a human adrenal gland cDNA library. NHP nucleotides
X are useful for drug screening and clinical trial monitoring, and for the
X diagnosis and treatment of physiological or behavioural disorders, cancer
X and infectious disease. Nucleotide constructs encoding functional NHPs,
X mutant NHPs, as well as antisense and ribozyme molecules can also be used
X in gene therapy for the modulation of NHP expression. NHP polypeptides
X may be used to produce agonists, antagonists and antibodies for the
X regulation of NHP expression in the treatment and/or diagnosis of
X disease.
X
X Sequence 1290 BP; 276 A; 438 C; 343 G; 230 T; 3 other;
Query Match 62.9%; Score 1143.4; DB 22; Length 1290;
Best Local Similarity 93.4%; Pred. NO. 0;
Matches 1224; Conservative 3; Mismatches 29; Indels 55; Gaps 1;

b 1115 TAAAG----- 1120
y 1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGGCA 1623
b 1121 -GAATCTTCACTTGACTCAGTCAAGAAAGTCAAGAAAGCAACTTCCAGAAAGGCA 1179
y 1624 CAGCACTTCGACTGCTCTGCTGGCCCCCAGAAAGTCACTGGAAAGCTTCTTAGCCGAG 1683
y 1180 CAGCACTTCGACTGCTCTGCTGGCCCCCAGAAAGTCACTGGAAAGCTTCTTAGCCGAG 1239
y 1684 ACCCTGGAGCTGAAGGTACGCGCCAGTCCAGACAAAGTGAACCAAGACATAA 1734
y 1240 ACCCTGGAGCTGAAGGTACGCGCCAGTCCAGACAAAGTGAACCAAGACATAA 1290

RESULT 34

AF84776

AAAF84776 standard; DNA; 1515 BP.

AAAF84776;

09-JUL-2001 (first entry)

Nucleotide sequence of a human chordin-like homologue splice variant.

Splice variant; chordin like homologue; CLH; bone modelling; bone injury;
von-Willebrand factor type C repeat; VWF repeat; bone formation;
reproductive disease; sexual differentiation; miscarriage; tumour;
sexual hormone; cardiovascular disorder; neuronal disease;
neurodegenerative disease; neuron development; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 265..1443

/*tag= a

/product= "chordin-like homologue splice variant"

WO200134796-A1.

17-MAY-2001.

10-NOV-2000; 2000WO-IL00736.

10-NOV-1999; 99IL-0132846.

28-DEC-1999; 99IL-0133767.

(COMP-) COMPUEN LTD.

Toporoff A, Biton S, Savitzky K, Bernstein J;

WPI; 2001-308783/32.

P-PSDB; AAB68079.

Nucleic acids encoding splice variants of a chordin like homologue,
useful in the treatment of bone injuries, diseases involved with the
female reproductive tract, diseases involving sexual hormone
abnormalities and cardiovascular disorders -

Claim 1; page 181-182; 203pp; English.

The present sequence encodes a splice variant of a chordin like
homologue (CLH). The protein is a homologue to the known chordin within
the von-Willebrand factor type C (VWF) domain repeat, which is found 2-4
times in these multi-domain proteins. The present protein contains 2
VWF repeats. CLH proteins and polynucleotides can be used for the
treatment of diseases which can be ameliorated, cured or prevented by
raising the level of a CLH. The nucleic acids, expression vectors,
proteins and antibodies are useful in the treatment of a disease selected
from diseases manifested in non-normal bone formation and non-normal bone
modelling, bone injuries, diseases involved with the female reproductive
tract, diseases of disorders involved with abnormal sexual

CC differentiation, recurrent miscarriages, tumours of the uterus, breast
CC or prostate, diseases involving sexual hormone abnormalities,
CC cardiovascular disorders, neural diseases of the CNS (central nervous
CC system), or neurodegenerative diseases and diseases involving non-normal
CC developments of neurons.

SQ Sequence 1515 BP; 378 A; 448 C; 404 G; 285 T; 0 other;

Query Match 62.7%; Score 1139.2; DB 22; Length 1515;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1141; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 674 TGTGAACTCACAACCTCTGGACTCCGGGCCCCCAACAAAGTCTCCAGCAACAACGG 733

DB 372 TCAGAACTCCACACTCCCTCTGGACTCCGGGCCCCCAACAAAGTCTCCAGCAACAACGG 431

QY 734 GACCATGTACCAACAGGAGAGATCTTCAGTGGCCATGAGCTGTTCCTCCCTCCGCTGCC 793

DB 432 GACCATGTACCAACAGGAGAGATCTTCAGTGGCCATGAGCTGTTCCTCCCTCCGCTGCC 491

QY 794 CAACAGTGTCTCTTGAGCTGCAAGAGGGCAGATCTACTCGGCTCTCAACAGCTG 853

DB 492 CAACAGTGTCTCTTGAGCTGCAAGAGGGCAGATCTACTCGGCTCTCAACAGCTG 551

QY 854 CCCCAGAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTCTGCCAAGCTGCCAA 913

DB 552 CCCCAGAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTCTGCCAAGCTGCCAA 611

QY 914 AGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGCTGAG 973

DB 612 AGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGCTGAG 671

QY 974 ACATCTCAGAGTCCATGTTCCAGTGTCTGGAGAAAGAGAGCCCGGACCCCGAGC 1033

DB 672 ACATCTCAGAGTCCATGTTCCAGTGTCTGGAGAAAGAGAGCCCGGACCCCGAGC 731

QY 1034 CCCCAGTGGCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTTCAGAGCCAAAGGAGC 1093

DB 732 CCCCAGTGGCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTTCAGAGCCAAAGGAGC 791

QY 1094 AGGCAGCAACAATCTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCTGTGTGATGG 1153

DB 792 AGGCAGCAACAATCTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCTGTGTGATGG 851

QY 1154 CGGAGAGACGTACTCCACGGGAGGTGTGSCACCGGCTTCGTGCTCTCGGCCCTT 1213

DB 852 CGGAGAGACGTACTCCACGGGAGGTGTGSCACCGGCTTCGTGCTCTCGGCCCTT 911

QY 1214 GCTCTGATCTTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGCGTGTGACTGTCC 1273

DB 912 GCTCTGATCTTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGCGTGTGACTGTCC 971

QY 1274 CACGAGTACCCCTCGCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCC 1333

DB 972 CACGAGTACCCCTCGCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCC 1031

QY 1334 AGAGAGCAAAAGACAGCCCTGGSCACAGTGAGATCAGTCTTACCAAGTGTGCCAAGCAC 1393

DB 1032 AGAGAGCAAAAGACAGCCCTGGSCACAGTGAGATCAGTCTTACCAAGTGTGCCAAGCAC 1091

QY 1394 GGGCGGGTCTCTGTCACACATCGGTATCCCGAGCCGAGACACCTGGCTGGCTTCC 1453

DB 1092 GGGCGGGTCTCTGTCACACATCGGTATCCCGAGCCGAGACACCTGGCTGGCTTCC 1151

QY 1454 CTTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTTGGAAAGCTGGTAAAGATGA 1513

DB 1152 CTTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTCTTGGAAAGCTGGTAAAGATGA 1211

QY 1514 GGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAAATCTTC 1573

DB 1212 GGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAAATCTTC 1271

QY 1574 ACTTGACTCAGATCAAGAAAGTCAAGAAAGCAAGACTTCCAGAAAGAGGACAGCACTTCC 1633

1514 GGAACTGAGGCTCAGAGAGGTGAGTACTGGGCCCAAGGCCACACAGCCAGATCTTCC 1573.
1213 GGAACTGAGGCTCAGAGAGGTGAGTACTGGGCCCAAGGCCACACAGCCAGAT-TTCC 1271
1574 ACTTGACTCAGATCAAGAAAGTCAGGAAGCAGAGACTTCCAGAAAGGCACAGCACTTCC 1633
1272 ACTTGACTCAGATCAAGAAAGTCAGGAAGCAGAGACTTCCAGAAAGGCACAGCACTTCC 1331
1634 GACTGCTCGCTGGCCCCCAGCAAGAGTCACTGGAAGCTTCTTCTAGCCAGACCCCTGGAGC 1693
1332 GACTGCTCGCTGGCCCCCAGCAAGAGTCACTGGAAGCTTCTTCTAGCCAGACCCCTGGAGC 1391
1694 TGAAGGTCAAGGCTGAGGCTCAGAGCAAGAGTGAACAGATCAACAGAGCTCAAGATTGCA 1753
1392 TGAAGGTCAAGGCTGAGGCTCAGAGCAAGAGTGAACAGATCAACAGAGCTCAACAGATTGCA 1451
1754 GATATGAGCTGTATTAATTTGTTGTTATATATATATTAATAAAGAGTTGCATTAACCATC 1813
1452 GATATGAGCTGTATTAATTTGTTGTTATATATATATTAATAAAGAGTTGCATTAACCATC 1511
1814 AAAA 1817
1512 AAAA 1515

RESULT 36
BQ61159
D ABO61159 standard, cDNA; 1373 BP.
X X
X ABO61159;
T 26-FEB-2003 (first entry)
E X
X Chordin-like homologue splice variant encoding sequence.
W X
W Neuroprotective; immunomodulator; cancer; chromosome 11;
W cytosolic; anti-inflammatory; gene therapy; nutritional supplement;
W wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
W amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
W vulnary; gene; ss.
X X
X Homo sapiens.
X W0200231111-A2.
X N
X 18-APR-2002.
X D
X 11-OCT-2001; 2001WO-US27760.
X F
X 12-OCT-2000; 2000US-0687527.
X R
X (HYSE-) HYSEQ INC.
X A
X Tang YT, Liu C, Zhou P, Auandi V, Zhang J, Zhao QA, Ren F;
I Xue AJ, Yang Y, Wehrman T, Drmanac RT;
R N-PSDB; ABF43915.
X R
X WPI; 2002-426278/45.
X T
X New polypeptides and their encoded proteins, useful as nutritional
T sources or supplements, or in gene therapy, particularly for treating
T wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
T inflammation -
T
T Claim 1; SEQ ID # 372; 357pp + sequence listing; English.
X X
X The invention relates to 446 newly isolated polynucleotide sequences.
C The activity of polynucleotides of the invention may be described as,
C vulnary, neuroprotective, immunomodulator, cytosolic and
C anti-inflammatory. Compositions comprising nucleic acids of the invention
C are useful for treating a mammalian subject, or as nutritional sources or
C supplements. These are useful in gene therapy, particularly for treating

CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records
CC AB060788-AB061233 represent polynucleotides of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1373 BP; 308 A; 447 C; 363 G; 255 T; 0 other;
Query Match 57.18; Score 1038.4; DB 24; Length 1373;
Best Local Similarity 99.98; Pred. No. 1.4e-286;
Matches 1039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 470 AGCCCCAGACATGTTCTTTCATGGAAGAGATATCTCCCGCGGAGAGCTGGCA 529
DB 187 ATGCCAGACATGTTCTTTCATGGAAGAGATATCTCCCGCGGAGAGCTGGCA 246
QY 530 CCCTACTTGGAGCACAAGGCTGATGTACTGCTGCTGTACCTGTCTAGAGGGCGC 589
DB 247 CCCTACTTGGAGCACAAGGCTGATGTACTGCTGCTGTACCTGTCTAGAGGGCGC 306
QY 590 CCATGTGAGTTGTTACCGCTCCACTGTCCGCTGTCTCACTGCCCGCAGCTGTGACGGA 649
DB 307 CCATGTGAGTTGTTACCGCTCCACTGTCCGCTGTCTCACTGCCCGCAGCTGTGACGGA 366
QY 650 GCCACAGCATGCTGTCTCCAGTGTGTGGAACCTTACACTCCCTCTGGACTCCGGGCCCC 709
DB 367 GCCACAGCATGCTGTCTCCAGTGTGTGGAACCTTACACTCCCTCTGGACTCCGGGCCCC 426
QY 710 ACCAAGTCTTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 769
DB 427 ACCAAGTCTTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 486
QY 770 TGAGCTGTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 829
DB 487 TGAGCTGTCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 546
QY 830 GATCTACTGGGCGCTCAGACCTGCGCCGACAGGCTGCCAGACCCCTCCCGCTCCCG 889
DB 547 GATCTACTGGGCGCTCAGACCTGCGCCGACAGGCTGCCAGACCCCTCCCGCTCCCG 606
QY 890 AGACTCTCTGCGCAAGCTGTCAAAGATGAGCGCAAGTGTGATGATGGAAGAGGACAG 949
DB 607 AGACTCTCTGCGCAAGCTGTCAAAGATGAGCGCAAGTGTGATGATGGAAGAGGACAG 666
QY 950 TGTGAGTCTGCTTCCATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAG 1009
DB 667 TGTGAGTCTGCTTCCATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAG 726
QY 1010 AAGAGAGGCGCGGGCACCCGACCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 1069
DB 727 AAGAGAGGCGCGGGCACCCGACCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 786
QY 1070 TGCCCACTTCAAGCCAGAGGAGCGGACGACAACTGTCAAGATGCTCTTGAAGAGAA 1129
DB 787 TGCCCACTTCAAGCCAGAGGAGCGGACGACAACTGTCAAGATGCTCTTGAAGAGAA 846
QY 1130 ACATAGAAAGCTGTGTGCAATGGCGGAAGACCTTCTCCACGCGGAGGTTGGCACCC 1189
DB 847 ACATAGAAAGCTGTGTGCAATGGCGGAAGACCTTCTCCACGCGGAGGTTGGCACCC 906
QY 1190 GGCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1249
DB 907 GGCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 966
QY 1250 GGCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1309
DB 967 GGCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1026
QY 1310 TGGGAGTGTCTGCAAGATTGCGGAGGACAAAGAGACCTTGGGACAGTGTGAGATCAG 1369

Db 1027 TGGGAAGTGTCTGAAGATTTCGCCACAGAGCAAAAGCAGACCTGGCCACAGTGAGATCAG 1086
ABK12125
Qy 1370 TTCTACAGGTGTCCCAAGGACCGGGCCGGGTCTCTGTCCACATCGGTATCCCCAAG 1429
Db 1087 TTCTACAGGTGTCCCAAGGACCGGGCCGGGTCTCTGTCCACATCGGTATCCCCAAG 1146
2y 1430 CCAGACACACCTGGCTCGCTTTCCTCCCTGGAAACACAGAGCCTCGGACTGGTGGAGACTTA 1489
Db 1147 CCAGACACACCTGGCTCGCTTTCCTCCCTGGAAACACAGAGCCTCGGACTGGTGGAGACTTA 1206
2y 1490 CCTCTGGAAGCTGGTAAAG 1509
Db 1207 CCTCTGGAAGCTGGTAAAG 1226
RESULT 37
ID ABK12125 standard; cDNA; 1517 BP.
AC ABK12125;
NC ABK12125;
XX 05-JUN-2002 (first entry)
DI Human cDNA encoding chordin homologue LP233.
DE Human; ss; gene; chordin homologue; LP233; neurological disorder;
KW Alzheimer's disease Parkinson's disease; wound; tissue repair;
KW bone fracture; spinal cord injury; pressure ulcer; diabetic ulcer;
KW venous stasis ulcer; burn; cardiovascular disorder; atherosclerosis;
KW thrombosis; heart failure; proliferative disorder; osteosarcoma;
KW breast cancer; leukaemia; prostate cancer; bone mineral density disorder;
KW osteopaenia-related disorder; fibrotic disorder; cirrhosis;
KW chronic asbestosis; restenosis; Gaucher's disease; Marfan's disease;
KW anaemia; diabetes mellitus; osteoporosis; transgenic.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT misc_feature 234..720
FT FT /*tag= a
FT /*note= "This region is specifically claimed in claim 2"
CDS 235..723
FT FT /*tag= b
FT /*product= "LP233"
FT sig_peptide 235..315
FT FT /*tag= c
FT misc_feature 315..720
FT FT /*tag= d
FT /*note= "This region is specifically claimed in claim 2"
FT mat_peptide 316..720
FT FT /*tag= e
FT /*label= Mature_LP233
XX WO200208277-A2.
PN
XX 31-JAN-2002.
XX
XX 05-JUL-2001; 2001WO-US16517.
XX
XX 19-JUL-2000; 2000US-219359P.
PR 04-MAY-2001; 2001US-288922P.
XX
XX (EJIL) LILLY & CO ELI.
PA
PI Alvarez E, McEntire JK, Smith RC, Su EW;
DR WPI; 2002-280599/32.
DR P-PSDB; AAU78173.
XX Novel isolated LP polypeptide having significant sequence similarity to
PT cysteine-rich regions of chordin, useful for treating neurological,
PT cardiovascular, proliferative fibrotic and osteopaenia-related disorders
PT

xx
ps
xx
cc The invention relates to isolated LP polypeptides (which have
cc significant sequence similarity to the cysteine-rich regions of chordin
cc being LP226, LP233 and LP236) and encoding polynucleotides. The
cc mature portions of the LP proteins and the region of the nucleic acid
cc encoding them are also included. Also included are a vector
cc comprising the polynucleotide, a host cell comprising the vector, an
cc anti-LP antibody and anti/agonists of the LP proteins. LP is useful in the
cc manufacture of a medicament. LP, LP polynucleotide Agonists or
cc antagonists of LP are useful for diagnosis and treatment of a
cc neurological disorder (e.g. Alzheimer's disease and
cc Parkinson's disease), a disorder requiring wound or tissue repair (where
cc the disorder is selected from bone fracture, spinal cord injury, pressure
cc ulcer, diabetic ulcer, venous stasis ulcer, and burn), a cardiovascular
cc disorder (e.g. atherosclerosis, thrombosis and heart failure), a
cc proliferative disorder such as osteosarcoma, breast cancer, leukaemia
cc and prostate cancer, a disorder associated with loss of bone mineral
cc density, an osteopaenia-related disorder, or a fibrotic disorder
cc (e.g. cirrhosis and chronic asbestosis) restenosis, Gaucher's disease,
cc Marfan's disease, anaemia, diabetes mellitus, osteoporosis and many other
cc diseases and disorders listed in the specification. LP is useful for
cc identifying compounds that bind to LP, and to isolate correlative
cc ligands. LP polynucleotide as hybridisation probes, in chromosome and
cc gene mapping and in the generation of antisense RNA and DNA, for the
cc preparation of LP, for generating either transgenic or knock out animals,
cc and for chromosome identification. The antibody is useful in diagnostic
cc assays for LP, for affinity purification of LP and as diagnostic and
cc therapeutic agent. The present sequence encodes the LP protein LP233.
xx
SQ Sequence 1517 BP; 314 A; 510 C; 379 G; 314 T; 0 other;

Query Match 56.5%; Score 1026.4; DB 24; Length 1517;
Best Local Similarity 87.1%; Pred. No. 4.1e-283;
Matches 1214; Conservative 0; Mismatches 31; Indels 149; Gaps 2;
Qy 424 TTGGGCTGGAGCCTCCTGGGACTAAACATGGCACTGTCTGGTTTGCAGGCCCCAGACATGT 483
Db 269 TGGGACTGCGCTGCTCTGTTCCTCCCTGGACTCCAGCTCGAGCGGCCAGACATGT 328
Qy 484 TCTGCTTTTTCATGGAGAGATCTCCCGGCGAGAGCTGGCCCTCTCTTGAGC 543
Db 329 TCTGCTTTTTCATGGAGAGATCTCCCGGCGAGAGCTGGCCCTCTCTTGAGC 388
Qy 544 CACAAGCCTGATGTACTGCTGGGCTGTACTGTCTCAGAGGGGCCCATGTGAGTGT 603
Db 389 CACAAGCCTGATGTACTGCTGGGCTGTACTGTCTCAGAGGGGCCCATGTGAGTGT 448
Qy 604 ACCGCTCCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGCCACAGCAATGCT 663
Db 449 ACCGCTCCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGCCACAGCAATGCT 508
Qy 664 GTCCCAAGTGTGGAACTCACCTCCCTCTGGACTCCGGGCCCCCAAGTCTCTGCC 723
Db 509 GTCCCAAGTGTGGAACTCACCTCCCTCTGGACTCCGGGCCCCCAAGTCTCTGCC 568
Qy 724 AGCAACACGGGACCATGTATCACAACGAGAGATCTTCAGTCCCATGAGTGTCCCT 783
Db 569 AGCAACACGGGACCATGTATCACAACGAGAGATCTTCAGTCCCATGAGTGTCCCT 628
Qy 784 CCGGCTGCCCAACCAAGTGTCTCTCTGAGCTGCACAGAGGGGCCAGATCTATCTGCGGCC 843
Db 629 CCGGCTGCCCAACCAAGTGTCTCTCTGAGCTGCACA ----- 666
Qy 844 TCACAACCTGCCCGGCAACAGGCTGCCAGCACCCCTCCCGTCCAGACTCTCTGTGCC 903
Db 667 ----- 666
Qy 904 AGCCTGCAAGAGTAGGGCACTGAGGCAATCGGATGAAGGACAGTGTGAGTGCCTCC 963
Db 667 -----ATGAGGCAAGTAGGCACTGAGGCAATCGGATGAAGGACAGTGTGAGTGCCTCC 714

673 ATGTGAATGTTACGGCTCGCTGGCCACCCCTTCACTGCTCACAGCCCTGTGTGAGC 732
2y 652 CACAGCAATGCTGCTCCAGAGTGTGTGGAACCTCACACTCCCTGTGACATCCGGGCCCCAC 711
2y 733 CACAGCAATGCTGCTCCAGAGTGTGTGGAACCTCACACTCCCTGTGACATCCGGGCCCCAC 792
2y 712 CAAAGTCTTCAGCAGCAACCGGACCATGTACCAACAGGAGAGATCTTCACTGCGCCATG 771
2y 793 TAAAGTCTTCAGCAGCAACCGGACCATGTACCAACAGGAGAGATCTTCACTGCGCCATG 852
2y 772 AGCTGTTCCTCCCTCCCGCTGCCAACAGTGTGTCTCTGAGCTGCACAGAGGCCACGA 831
2y 853 AGCTGTTCCTCCCTCCCGCTGCCAACAGTGTGTCTCTGAGCTGCACAGAGGCCACGA 912
2y 832 TCTACTGCGGCTTCACAACTCCCGCCGAAACCGAGGTGCCACACCCCTCCCGCTGCCAG 891
2y 913 CTTACTGTGTCTATGACCTGTCTCTGAAACCCAGCTGCCACACACACTCCCTCTGCGCTG 972
2y 892 ACTCTCTGTCGAAGCTGCAAAAGATGAGCAAGTGTGCAATCGATGAGAGGACAGTG 951
2y 973 ATTCTCTGTCTGACCTCTGCAAGCAGCAGCACTGAGAGTTCCACAGAGAAACTTGA 1032
2y 952 TGCAGTCTCTCATGGGTGAGACATCTCTGAGATCCATGTTCCAGTGATGTGGGAGAA 1011
2y 1033 CACAGCTGTCAGCTGAGAGAGACATTCACAGATCCATGCTC-----GGAGA 1080
2y 1012 AGAGAGCCCGGACCCCGACCCCGCTCTGAGCTGAGAGCTGAGCTGATGCTGCTC 1071
2y 1081 GGAGAGCCCGGACCCCGACCCCGCTCTGAGCTGAGAGCTGAGCTGATGCTGCTC 1140
2y 1072 GCCACTTCAGACCCAGGAGCAGCAGCAGCACTGTCAAGATCGTCTCAGAGAGAAAC 1131
2y 1141 GCCACTTCAGTCACTGAGTGGGAGGAGCAACACCATCAAGATTATCTTGAAGAGAAAC 1200
2y 1132 ATGAGAAGCTGTGTGATGGCGGAGAGCTGACCTCCAGCGGAGGTGTGCGACCCGG 1191
2y 1201 ATGAAAAGCTTCACACAAATGGGAGAGCACTATCCCATGGGAGGTGTGCGACCCCA 1260
2y 1192 CTTCTCGTGTCTTCGCGCCCTTGCCTGCTGCTTATGCACTGTGAGAGTGGCGCCAGG 1251
2y 1261 CTGTGCTCTCTTGTGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
2y 1252 AATGCGAGCTGTGACCTCTCCACAGGATACCCCTGCGCTCAACCCCGAGAAAGTGGCTG 1311
2y 1321 ACTGCCCGTGTGACCTGCGCCCGCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
2y 1312 GGAAGTGTGCAAGATTTCCCGAGAGGACAAAGCAGACCTTGGCCACAGTGAGATCAGTT 1371
2y 1381 GGAAGTGTGCAAGATTTCCCGAGAGGAGGAGGAGAGATGACACAGTGAGATCAGTT 1440
2y 1372 CTACAGAGTGTCCAGAGGACCGGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1431
2y 1441 CACCCGGTGTCCAGAGTACCGGCGGAGTTCGAGGTGACGTGCTGCTGCTGCTGCTGCTGCTG 1500
2y 1432 CAGACAACTGCGGTGCTTGGCTGCAACAGAGGCTGCGACTGTGCTGCTGCTGCTGCTGCTGCTG 1491
2y 1501 CAGACAGCTACACCGCTTGTCTGGAGCATGAAGCCTCTGACAGTAGAGATGTACA 1560
2y 1492 TCTGAGCTGTGTAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAA 1551
2y 1561 TTTGGAAGCTGGTGAAG----- 1578
2y 1552 GGCACACAGCCCAATCTTCCACTTGTACTCAGATCAAGAAAGTTCAGGAGCAGAGATTC 1611
2y 1579 -----GAATCTACCACTTGTGTTTCAATCAAGAGTTCAGGAGCAGAGATTC 1625
2y 1612 CAGAAAGGCGACAGCACTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1671
2y 1626 CAGAAAGGCTCAGAACTTTCGGCTGTCTGCGGCGCCCTGAGAGTTTCTGAGCCGCTC 1685
2y 1672 TTTCTAGCCCGAGCCCTGGAGCTGTAAGGTTCAGGCTCAGAGCAAAAGTGCACAGACA 1731
2y 1686 TTTCTAGCCCGAGCTCAGAGCTGTAAGTTTACGCGCCAGCAAAAGTGCACAGACA 1745

Qy 1732 TAAACAAGA-----CCTAACAGTTCAGATATAGCTGTATTAATTTGTTGTTATATATT 1787
Db 1746 TTATAGCAAGGACCTTAAAGAGTTTCAGATACGAGTTTATTTGGTTTGTATTATATATT 1805
Qy 1788 AATAAATAAG 1797
Db 1806 AATAAAGAG 1815

RESULT 39

AAZ41343/C
ID AAZ41343 standard; cDNA; 807 BP.

XX AAZ41343;

AC
XX
XX
DT 19-JAN-2000 (first entry)

XX Human normal uterus tissue derived cDNA 19.

XX Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
EST; expressed sequence tag; ss.

XX Homo sapiens.

OS
XX
XX
PN DE19817946-A1.

XX 21-OCT-1999.

XX 17-APR-1998; 98DE-1017946.

XX 17-APR-1998; 98DE-1017946.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
WPI; 1999-591956/51.
P-PSDB; AAY69887, AAY69888, AAY69889.

XX New nucleic acid sequences expressed in normal uterine tissues, and
derived polypeptides, for treatment of uterine cancer and
identification of therapeutic agents -

XX Claim 3; Page 86; 154pp; German.

XX This invention describes novel cDNA sequences (A) highly expressed in
normal uterine tissue which can have anticancer and cytostatic activity
and can be used for gene therapy. (A) are used (i) for recombinant
expression of polypeptides (B) and (ii) to isolate complete genes.
(B) are used (i) to identify agents suitable for treatment of uterine
cancer; (ii) directly for treating this form of cancer (including
expression from gene therapy vectors) and (iii) for generation of
specific antibodies. (A) are identified by assembling ESTs (expressed
sequence tags) from a particular tissue type before comparison of
expression patterns. This allows a significantly longer fragment of the
gene to be revealed, so should reduce the number of failures associated
with the fact that ESTs from different libraries may represent
different parts of the same unknown gene, distorting the estimated
frequency of occurrence in a particular tissue. AAZ41325-241385
represent the human uterine tissue derived cDNA fragments of the
invention which encode the protein fragments represented in
AAY59838-Y59892.

XX Sequence 807 BP; 149 A; 203 C; 252 G; 203 T; 0 other;

Query Match 37.2%; Score 675.4; DB 20; Length 807;

Best Local Similarity 91.3%; Pred. No. 9.6e-183;

Matches 784; Conservative 0; Mismatches 16; Indels 59; Gaps 4;

Qy 962 CGATGGCTGAGATCCCTCAGATCCCATGTT-CCATGATGCTGGAGAAAGAGAGGCC 1020
Db 804 CCACGGCTTAGACCCCTCAGCATCCCTGTTCCCATCCATCCTGGAGAAAGAGAGGCC 745

2Y 1021 CGGCG-ACCCGAGCCCCACATGGGCTCAGGGCCCTCTGAGCTTCATCCCTCGCCACTTC 1079
2b 744 CGGTGACACCCAGCCCCACATGGGCTCAGGGCCCTCTGAGCTTCATCCCTCGCCACTTC 685
2Y 1080 AGACCCAGGAGCAGGCGAGCACAACCTGTCAAGATCGTCTCAAGAGAGAAAATAGAAA 1139
2b 684 AGACCCAGGAGCAGGCGAGCACAACCTGTCAAGATCGTCTCAAGAGAGAAAATAGAAA 625
2Y 1140 GCCTGTGTGTCATGGCGGGAAGACGTAATCCACGGGAGAGGTGGGCAACCGGCCCTTCGGT 1199
2b 624 GCCTGTGTGTCATGGCGGGAAGACGTAATCCACGGGAGAGGTGGGCAACCGGCCCTTCGGT 565
2Y 1200 GCCTTCGGGCCCTTCGGCCCTGATCTATGACCTGTGAGATGGCCGCGAGCTGCCAG 1259
2b 564 GCCTTCGGGCCCTTCGGCCCTGATCTATGACCTGTGAGATGGCCGCGAGCTGCCAG 505
2Y 1260 CGTGTGACCTGTCCACCGAGTACCCCTCGCTGCAACCCGAGAAAGTGTGGGAAGTGC 1319
2b 504 CGTGTGACCTGTCCACCGAGTACCCCTCGCTGCAACCCGAGAAAGTGTGGGAAGTGC 445
2Y 1320 TGCAAGATTGGCCAGAGGACAAAGCAGACCCCTGGCCACAGTACGATTCTTACCAGG 1379
2b 444 TGCAAGATTGGCCAGAGGACAAAGCAGACCCCTGGCCACAGTACGATTCTTACCAGG 385
2Y 1380 TGTCCCAAGGACCGGGCCGGTCTCGTCCACACATCGGTATCCCAAA--GCCCGAGCA 1437
2b 384 TGTCCCAAGGACCGGGCCGGTCTCGTCCACACATCGGTATCCCAAAAGGCCCGAGCA 325
2Y 1438 ACCTGGCTGCTTTGCCCTGGAACAGAGGCTCGGACTGGTGGAGATCTACCTCTGGA 1497
2b 324 ACCTGGCTGCTTTGCCCTGGAACAGAGGCTCGGACTGGTGGAGATCTACCTCTGGA 265
2Y 1498 AGCTGTAAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCAC 1557
2b 264 AGCTGTAAAAG----- 253
2Y 1558 ACAGCCAGAACTTCTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAA 1617
2b 252 -----GAACTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAA 200
2Y 1618 GAGGACAGACTTCCGACTGCTCGTGGCCCGCCACAGAGTCACTGGAAGCTCTTCTTA 1677
2b 199 GAGGACAGACTTCCGACTGCTCGTGGCCCGCCACAGAGTCACTGGAAGCTCTTCTTA 140
2Y 1678 GCCCAGACCTGGAGCTGAAGGTCAAGGCCAGTCCAGCAAAAGTGCACCAAGACATAACAA 1737
2b 139 GCCCAGACCTGGAGCTGAAGGTCAAGGCCAGTCCAGCAAAAGTGCACCAAGACATAACAA 80
2Y 1738 AGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTATAATAAAG 1797
2b 79 AGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTATAATAAAG 20
2Y 1798 AAGTGTCAATACCATCAAA 1816
2b 19 AAGTGTCAATACCTCAAA 1

RESULT 40

AA575270/c

D AA575270 standard; cDNA; 622 BP.

X C

X C AA575270;

X T

X T 13-FEB-2002 (first entry)

X E

X E DNA encoding novel human diagnostic protein #11074.

X W

X W Human; chromosome mapping; gene mapping; gene therapy; forensic;

X W

X W food supplement; medical imaging; diagnostic; genetic disorder; ss.

X S

X S Homo sapiens.

PN WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG11083.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX Claim 1; SEQ ID No 11074; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences (II) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) as useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AA564197-AA594584 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: the sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 622 BP; 115 A; 155 C; 170 G; 182 T; 0 other;
Query Match 29.9%; Score 543.6; DB 23; Length 622;
Best Local Similarity 97.7%; Pred. No. 4.6e-145;
Matches 594; Conservative 0; Mismatches 9; Indels 5; Gaps 4;
QY 1215 CCTGTGATCCTATGACCTGTGAGGATGCGCCGAGGACTGCCAGAGCTGTGACCTGTCCC 1274
Db 622 CCATGATCTTATGACCTGTGAGGATGCGCCGAGGACTGCCAGAGCTGTGACCTGTCCC 563
QY 1275 ACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGCTGGGAAGTCTGCGAAGATTGGCCA 1334
Db 562 ACGAAGTACCCCTGCGGTACCCCTGAGATAGTGGCTGGGAAGTCTGCGAAGATTGGCCA 503
QY 1335 GAGGACAAAGCAGACCCCTGGCCACAGTACGATGATGATGATGATGATGATGATGATG 1394
Db 502 GAGGACAAAGCAGACCCCTGGCCACAGTACGATGATGATGATGATGATGATGATGATG 443
QY 1395 GCGCGGCTCTCGTCCACATCGGTATCCCAAGCCAGACAACTCGGTGCTGTGTC 1454
Db 442 GCGCGGCTCTCGTCCACATCGGTATCCCAAGCCAGACAACTCGGTGCTGTGTC 383
QY 1455 C--TGGAAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGTAAGATG 1512
Db 382 CTTGGGAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGTAAGATG 323
QY 1513 AGGAAAC-TGAGGCTCA-GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGATCT 1570

322 AGGAACTTGAGGCTCAGAGAGGTGAGTACCTGGCCCAAGGCCACACAGCCAGAATCT 263
1571 TCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAGACTT-CCAGAAAGAGGCACAGCAC 1629
262 TCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAGACTTCCCCAGAAAGAGGCACAGCAC 203
1630 TTCGAGCTGCTCGCTGGCCCCCAGGAGGTCACTGGRAGCTTCTCCTAGCCAGACCTG 1689
202 TTCGAGCTGCTCGCTGGCCCCCAGGAGGTCACTGGRAGCTTCTCCTAGCCAGACCTG 143
1690 GAGTGAAGGTCAAGCCAGTCCAGACAAAGTGACCAAGACATACAAAGACCTTAACAGT 1749
142 GAGTGAAGGTCAAGCCAGTCCAGACAAAGTGACCAAGACATACAAAGACCTTAACAGT 83
1750 TGCAGATATGAGCTGTATAATTGTTGTTATTATATATTATTAATAAAGAGTTGCATAAC 1809
82 TGCAGATATGAGCTGTATAATTGTTGTTATTATATATTATTAATAAAGAGTTGCATTAC 23
1810 CATCAAAA 1817
22 CCTCAAAA 15

Search completed: January 31, 2004, 01:00:37
Job time : 516 secs

PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14	PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105003

PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 73.9%; Score 1342.8; DB 11; Length 1732;
Best Local Similarity 79.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

2Y 424 TTGGGCTGGAGCCTCTCTGGGACTAAATGGGCACTGGTGGTGGTGGCCAGGCCCGAGACATGT 483
2b 321 TGGGACTCTGGGCTGTCTGGTTCCTCCCTGGGACTCCCACTGGAGCCGCGCCAGACATGT 380
2Y 484 TCTGGCTTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGCACCTCTACTTTGGAGC 543
2b 381 TCTGGCTTTTCCATGGGAAGAGATCTCCCGGGGAGAGCTGGCACCTCTACTTTGGAGC 440
2Y 544 CACAGGCTGATGATCTGCTGGCTGGTGTACCTGTCTCAGAGGGGCGCCATGTGAGTTGTT 603
2b 441 CACAGGCTGATGATCTGCTGGCTGGTGTACCTGTCTCAGAGGGGCGCCATGTGAGTTGTT 500
2Y 604 ACCGCTTCCACTGTCCGCTCTCCACTGGCCCGGAGCTGTGACGGAGCCACAGCAATGCT 663
2b 501 ACCGCTTCCACTGTCCGCTCTCCACTGGCCCGGAGCTGTGACGGAGCCACAGCAATGCT 560
2Y 664 GTCCCAAGTGTGGAACTCTCACACTCCCTCTGGACTCCGGGCGCCACCAAGTCTCTGCC 723
2b 561 GTCCCAAGTGTGGAACTCTCACACTCCCTCTGGACTCCGGGCGCCACCAAGTCTCTGCC 620
2Y 724 AGCAACGGGACCATGTACCAACAGGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 783
2b 621 AGCAACGGGACCATGTACCAACAGGAGATCTTCAGTGCCCATGAGCTGTTCCTCT 680
2Y 784 CCGGCTGCCCAACAGATGTGTCTTCAGCTGTCACAGAGGGCGAGATCTACTGGGCC 843
2b 681 CCGGCTGCCCAACAGATGTGTCTTCAGCTGTCACAGAGGGCGAGATCTACTGGGCC 740
2Y 844 TCACAACCTGCCCGGAAACAGGCTGCCAGCACCTCCCTCCGCTGCCAGACTCTCTGCC 903
2b 741 TCACAACCTGCCCGGAAACAGGCTGCCAGCACCTCCCTCCGCTGCCAGACTCTCTGCC 800
2Y 904 AAGCTCGAAGATGAGCAAGTGCAGCAATCGGATGAGAGAGCAGTGTGCTGCTGCC 963
2b 801 AAGCTCGAAGATGAGCAAGTGCAGCAATCGGATGAGAGAGCAGTGTGCTGCTGCC 860
2Y 964 ATGGGCTGAGACATCTCAGGATTCATGTTCCAGTGTGCTGGGAGAGAGAGGCGCGG 1023
2b 861 ATGGGCTGAGACATCTCAGGATTCATGTTCCAGTGTGCTGGGAGAGAGAGGCGCGG 920
2Y 1024 GCACCCAGCCCTCCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCATTCAGAC 1083
2b 921 GCACCCAGCCCTCCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCATTCAGAC 980
2Y 1084 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCTGCTGAGGAGAAACATAAGAAAGCT 1143
2b 981 CCAAGGAGCAGGAGCAGCAACTGTCAAGATCTGCTGAGGAGAAACATAAGAAAGCT 1040
2Y 1144 GTGGCTATGGGGGAGAGATCTCCACCGGGGAGTGGCACCGGCTCTCGTGGCT 1203
2b 1041 GTGGCTATGGGGGAGAGATCTCCACCGGGGAGTGGCACCGGCTCTCGTGGCT 1100
2Y 1204 TGGGCTCTTGGCTGATCTCTATGCACTGTGAGATGCGCGCCAGGACTGCGACGTG 1263
2b 1101 TGGGCTCTTGGCTGATCTCTATGCACTGTGAGATGCGCGCCAGGACTGCGACGTG 1160
2Y 1264 TGACCTGTCCACCGAGTACCTCTCGCTCCAGCCCGGAGAAAGTGGCTGGGAGTGTGCA 1323

Db 1161 TGACCTGTCCACCGAGTACCTCTCCGCTGACCCCGAGAAAGTGGCTGGAGAGTGTGCA 1220
Qy 1324 AGATTTGCCCAGAGGACAAAGAGACA CCGTGGGCCACAGTGAGATCAGTTCTA CCAAGTGTG 1383
Db 1221 AGATTTGCCCAGAGGACAAAGAGACA CCGTGGGCCACAGTGAGATCAGTTCTA CCAAGTGTG 1280
Qy 1384 CCAAGGACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCAGACAAACCTGC 1443
Db 1281 CCAAGGACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCAGACAAACCTGC 1340
Qy 1444 GTGCTTTGCCCTGGAA CACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1503
Db 1341 GTGCTTTGCCCTGGAA CACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGG 1400
Qy 1504 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCCACTTCAGTCAAGATCAAGAAAGTCAAGAGCAAGTCTCCAGAAAGGCA 1623
Db 1461 AGAATCTTCCACTTCAGTCAAGATCAAGAAAGTCAAGAGCAAGTCTCCAGAAAGGCA 1520
Qy 1624 CAGCACTTCGCACTGCTGGTGGCCCGCCACAGAGTCACTGGAACTGTTCTCTAGCCAG 1683
Db 1521 CAGCACTTCGCACTGCTGGTGGCCCGCCACAGAGTCACTGGAACTGTTCTCTAGCCAG 1580
Qy 1684 ACCCTGGAGTGAAGTCA CCGCCAGTCCAGCAAGTGA CCAAGTGA CCAAGTGA CCAAGTGA 1743
Db 1581 ACCCTGGAGTGAAGTCA CCGCCAGTCCAGCAAGTGA CCAAGTGA CCAAGTGA CCAAGTGA 1640
Qy 1744 AACAGTTCAGATGAGCTGTATATTTGTTTATTATTTATTAATTAATTAATTAATTAATTA 1803
Db 1641 AACAGTTCAGATGAGCTGTATATTTGTTTATTATTTATTAATTAATTAATTAATTAATTA 1700
Qy 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCTCAAAA 1714

RESULT 3
US-10-011-795A-141
; Sequence 141, Application US/10011795A
; Publication No. US20040005626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/011.795A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 141
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-011-795A-141

Query Match 73.9%; Score 1342.8; DB 12; Length 1732;

784 CCGGCTCCCAACAGTGTGCTCTCTGAGTGCACAGAGGSCCAGATCTACTGGGCC 843
b CCGGCTCCCAACAGTGTGCTCTCTGAGTGCACAGAGGSCCAGATCTACTGGGCC 740
Y TCAACACTGTCGCCGACAGAGTGCACAGAGGSCCAGATCTACTGGGCC 903
b TCAACACTGTCGCCGACAGAGTGCACAGAGGSCCAGATCTACTGGGCC 800
Y AGACTGCAAGATGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 963
b AGACTGCAAGATGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 860
Y ATGGGGTGAAGATCTCTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 1023
b ATGGGGTGAAGATCTCTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 920
Y GACACCCAGCCCACTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 1083
b GACACCCAGCCCACTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 980
Y CCAGGGAGAGGAGGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1143
b CCAGGGAGAGGAGGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1040
Y GTGTGATGGGGGAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1203
b GTGTGATGGGGGAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1100
Y TGGGCCCCCTTGGCTGATCTATGACATCTGAGGATGCGCGCCAGGACTGCCAGCGT 1263
b TGGGCCCCCTTGGCTGATCTATGACATCTGAGGATGCGCGCCAGGACTGCCAGCGT 1160
Y TGACTGTGTCACAGGATGTCCTGTCACCCGAGAGAGTGCCTGGAGGTCGCA 1323
b TGACTGTGTCACAGGATGTCCTGTCACCCGAGAGAGTGCCTGGAGGTCGCA 1220
Y AGATTGGCCAGAGGAGGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1383
b AGATTGGCCAGAGGAGGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1280
Y CCAAGGCAACCGGCGGGTCTGTCACACATCGGTATCCCAAGCCCAAGCAACTGC 1443
b CCAAGGCAACCGGCGGGTCTGTCACACATCGGTATCCCAAGCCCAAGCAACTGC 1340
Y GTGGCTTTGCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTGGAAGCTG 1503
b GTGGCTTTGCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACTGGAAGCTG 1400
Y TAAAGATGAGGAACTGAGGCTCAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1563
b TAAAGATGAGGAACTGAGGCTCAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1460
Y AGAATCTTCCATTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1623
b AGAATCTTCCATTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1520
Y CAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1683
b CAGCACTTCCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1580
Y ACCCTGGAGCTGAGAGTCAAGGCTCAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1743
b ACCCTGGAGCTGAGAGTCAAGGCTCAGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 1640
Y ACAGTTGCAATATGAGTGTATTAATTTGTTTATTAATTAATTAATTAATTAATTAATTAAT 1803
b ACAGTTGCAATATGAGTGTATTAATTTGTTTATTAATTAATTAATTAATTAATTAATTAAT 1700
Y CATAACCATCAAAA 1817
b CATTACCCCTCAAAA 1714

RESULT 6
US-10-063-735-81
; Sequence 81, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 81
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-735-81

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCTCTCTGGGACTTAACATGGGACTGGTGGCTTTGGCCAGGSCCCAGACATGT 483
Db TGGGACTCGGCTGCTCTGGTTCCTCCCTGGACTCCAGCTCGAGCGCCGACGACATGT 380
QY 484 TCTGCTTTTTCATGGGAGAGATCTCCCGGAGAGCTGGGACCCCTACTTGGAGC 543
Db TCTGCTTTTTCATGGGAGAGATCTCCCGGAGAGCTGGGACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
Db CACAAGGCTGATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 604 ACCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db ACCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Db GTCCCAAGTGTGGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 724 AGCAACAGGAGCTGATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
Db AGCAACAGGAGCTGATGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
QY 784 CCGGCTTCCCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
Db CCGGCTTCCCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 844 TCACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
Db TCACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 904 AGGCTGCAAGATGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 963
Db AGGCTGCAAGATGAGGAGTGCACAGAGGSCCAGATCTACTGGGCC 860
QY 964 ATGGGGTGAAGATCTCTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 1023
Db ATGGGGTGAAGATCTCTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 920
QY 1024 GCACCCCAAGCCCACTGAGGATCCATGTTCCAGTGTGTCGGGAAAGAGAGGCCCG 1083

921 GCACCCGAGCCCACTGGCTCAGGCGCCCTCTGAGCTTCATCCCTGCCACTTCAGAC 980
1084 CCAAGGAGCAGGCGAGCAACACTGCAAGATCGTCTCAAGGAGAAACATAAGAAAGCCT 1143
981 CCAAGGAGCAGGCGAGCAACACTGCAAGATCGTCTCAAGGAGAAACATAAGAAAGCCT 1040
1144 GTGTGCATGCGGGAGAGCAGTACTCCACGCGGAGGTGTGACACCGGCTTCCGTGCT 1203
1041 GTGTGCATGCGGGAGAGCAGTACTCCACGCGGAGGTGTGACACCGGCTTCCGTGCT 1100
1204 TCGGCCCCCTTGCCTGCACTCTATGACACTGTGAGATGGCGCCAGGACTCCAGCTG 1263
1101 TCGGCCCCCTTGCCTGCACTCTATGACACTGTGAGATGGCGCCAGGACTCCAGCTG 1160
1264 TGACCTGTGCCACGAGTACCCCTGCGCTCACCCGAGAAAGTGCGTGGAAAGTCTGCA 1323
1161 TGACCTGTGCCACGAGTACCCCTGCGCTCACCCGAGAAAGTGCGTGGAAAGTCTGCA 1220
1324 AGATTTCCACAGAGCAAAAGCAGACCTCGGCCACAGTGAGATCACTTACCAAGTGT 1383
1221 AGATTTCCACAGAGCAAAAGCAGACCTCGGCCACAGTGAGATCACTTACCAAGTGT 1280
1384 CCAAGGACCGGCGCGGCTCTGCTCCACACATCGGTATCCCAAGCCAGACCAACCTGC 1443
1281 CCAAGGACCGGCGCGGCTCTGCTCCACACATCGGTATCCCAAGCCAGACCAACCTGC 1340
1444 GTCGCTTTGCCCTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACTCTGAGAGCTGG 1503
1341 GTCGCTTTGCCCTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACTCTGAGAGCTGG 1400
1504 TAAAGATGAGGAAACTGAGCTCAGAGAGGTGAAGTACTGGGCCCAAGGCCACAGCC 1563
1401 TAAAGATGAGGAAACTGAGCTCAGAGAGGTGAAGTACTGGGCCCAAGGCCACAGCC 1460
1564 AGATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGCA 1623
1461 AGATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGCA 1520
1624 CAGCACTTCGAGCTGCTGCTGGCCCCCAGAGGCTCACTGGAAGCTTCTTAGCCAG 1683
1521 CAGCACTTCGAGCTGCTGCTGGCCCCCAGAGGCTCACTGGAAGCTTCTTAGCCAG 1580
1684 ACCCTGAGCTGAAGTCAAGCGCCAGTCCAGACAAAGTGAAGCAAGATCAAGAGCT 1743
1581 ACCCTGAGCTGAAGTCAAGCGCCAGTCCAGACAAAGTGAAGCAAGATCAAGAGCT 1640
1744 AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATTAATAATAAAGAGTTG 1803
1641 AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATTAATAATAAAGAGTTG 1700
1804 CATACCATCAAAA 1817
1701 CATATCCCTCAAAA 1714

RESULT 7
US-10-006-130A-141
; Sequence 141, Application US/10006130A
; Publication NO. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James
; APPLICANT: Paoletti, Nicholas F.
; TITLE OF INVENTION: Secretion and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 141
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-130A-141
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCTCTCTGGGACTAAATGGCACTGGTGGTTTGCAGGCCGAGACATGT 483
DB 321 TGGGACTCGCGCTGTCTGGTTCCCTCGGACTCCACGCTCGAGCGCCGCGGAGATGT 380
QY 484 TCTGCTTTTCCATGAGGAGAGATACCTCCCGGCGAGAGCTGCGACCCCTATCTGGAGC 543
DB 381 TCTGCTTTTCCATGAGGAGAGATACCTCCCGGCGAGAGCTGCGACCCCTATCTGGAGC 440
QY 544 CACAAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
DB 441 CACAAGGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 604 ACCGCTTCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
DB 501 ACCGCTTCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAACTCACTCTCTGAGACTCCGCGGCCCAACCAATCTGCTGCTGCTGCT 723
DB 561 GTCCCAAGTGTGGAACTCACTCTCTGAGACTCCGCGGCCCAACCAATCTGCTGCTGCTGCT 620
QY 724 AGCAAAACGGGAGCACTGTATACCAACAGAGAGATCTTCACTGCTGCTGCTGCTGCTGCTGCT 783
DB 621 AGCAAAACGGGAGCACTGTATACCAACAGAGAGATCTTCACTGCTGCTGCTGCTGCTGCTGCT 680
QY 784 CCGGCTGCGCCACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 681 CCGGCTGCGCCACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 844 TCAAACTGCTGCGCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
DB 741 TCAAACTGCTGCGCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 904 AAGCCTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGAGTGTGCTGCTGCT 963
DB 801 AAGCCTGCAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGAGTGTGCTGCTGCT 860
QY 964 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023
DB 861 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
QY 1024 GCACCCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
DB 921 GCACCCGAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
QY 1084 CCAAGGAGCAGGCGAGCAACACTGTGAAGATCGTCTGAGAGGAGAACTAAGAAAGCCT 1143
DB 981 CCAAGGAGCAGGCGAGCAACACTGTGAAGATCGTCTGAGAGGAGAACTAAGAAAGCCT 1040
QY 1144 GTGTGCATGCGGGAGAGCAGTACTCCACGCGGAGGTGTGACACCGGCTTCCGTGCTGCT 1203
DB 1041 GTGTGCATGCGGGAGAGCAGTACTCCACGCGGAGGTGTGACACCGGCTTCCGTGCTGCT 1100
QY 1204 TCGGCCCCCTTGCCTGCACTCTATGACACTGTGAGATGGCGCCAGGACTCCAGCTG 1263

1101 TCAGCCCTTGGCCCTGCACTCTATGCACTGTAGAGATGGCCGCGAGGACTGCCAGCGTG 1160
1264 TGACCTGTCCACCGAGTACCCCTGCCGTCAACCCGGAAGAGTGGCTGGAAAGTCTGCA 1323
1161 TGACCTGTCCACCGAGTACCCCTGCCGTCAACCCGGAAGAGTGGCTGGAAAGTCTGCA 1220
1324 AGATTGGCCGAGGACAAAGACAGACCCCTGGCCACAGTGTCTTACCAAGGTGTC 1383
1221 AGATTGGCCGAGGACAAAGACAGACCCCTGGCCACAGTGTAGTCACTTACCAAGGTGTC 1280
1384 CCAAGGACCGGGCGGGTCTCGTCCACACATCGGTATCCCAAGCCCGAGACCACTGC 1443
1281 CCAAGGACCGGGCGGGTCTCGTCCACACATCGGTATCCCAAGCCCGAGACCACTGC 1340
1444 GTGCTTTGCCCTGGAACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAAGTGG 1503
1341 GTGCTTTGCCCTGGAACAGAGGCTCGGACTTGGTGGAGATCTACTCTGGAAAGTGG 1400
1504 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGCCACACAGCC 1563
1401 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGCCACACAGCC 1460
1564 AGAATCTTCCACTTGATCAGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGGCA 1623
1461 AGAATCTTCCACTTGATCAGATCAAGAAAGTCAAGAGCAAGACTTCCAGAAAGGCA 1520
1624 CAGCACTTCGAGTGTCTGCTGCGCCCGCCAGAGGTCACTGGAAGTCTTCTAGCCAG 1683
1521 CAGCACTTCGAGTGTCTGCTGCGCCCGCCAGAGGTCACTGGAAGTCTTCTAGCCAG 1580
1684 ACCTGGAGCTGAAGGTCAAGGCTCAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGCT 1743
1581 ACCTGGAGCTGAAGGTCAAGGCTCAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGCT 1640
1744 AACAGTTGAGATGAGCTGTATTAATTTGTTTATTATATATTAATTAATTAAGAGTTG 1803
1641 AACAGTTGAGATGAGCTGTATTAATTTGTTTATTATATATTAATTAATTAAGAGTTG 1700
1804 CATAACCAATAA 1817
1701 CATTACCTCAAA 1714

RESULT 8

S-10-199-672-281
Sequence 281, Application US/10199672
Publication No. US2003014842A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C
CURRENT APPLICATION NUMBER: US/10/199,672
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 2002-07-18
PRIORITY FILING DATE: 2002-01-15
PRIORITY FILING DATE: 2002-01-15
PRIORITY FILING DATE: 1997-09-18
PRIORITY FILING DATE: 1997-09-18
PRIORITY FILING DATE: 1997-09-18
PRIORITY FILING DATE: 1997-10-17
PRIORITY FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-199-672-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGGCTCTGGGACTAAATGCGACTGTGGCTTTGGCCAGGCCCCAGACATGT 483
DB 321 TGGGACTCGGCTGCTGTGGTTCCCTCGGACTCCGACTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCCCTTTTCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCAACCTTACTTTGGAGC 543
DB 381 TCTGCCCTTTTCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCAACCTTACTTTGGAGC 440
QY 544 CACAAGGCTGTATGTACTGCTGCTGTACTGCTGTAGTCTCAGAGGGCGCCATGTGAGTTGTT 603
DB 441 CACAAGGCTGTATGTACTGCTGCTGTACTGCTGTAGTCTCAGAGGGCGCCATGTGAGTTGTT 500
QY 604 ACCGCTTCCACTGTCCGCTGTCCACTGCCGCCCACTGTGAGCGAGGCCACAGCAATGCT 663
DB 501 ACCGCTTCCACTGTCCGCTGTCCACTGCCGCCCACTGTGAGCGAGGCCACAGCAATGCT 560
QY 664 GTCCGAAGTGTGGAACTTCACTTCCCTGTGAGCTCCGCGGCCCAACCAAGTCTGCC 723
DB 561 GTCCGAAGTGTGGAACTTCACTTCCCTGTGAGCTCCGCGGCCCAACCAAGTCTGCC 620
QY 724 AGCACAACGGAGCAATGTATCAACACGAGAGATCTTCACTGCCCCATGAGCTGTGCCCT 783
DB 621 AGCACAACGGAGCAATGTATCAACACGAGAGATCTTCACTGCCCCATGAGCTGTGCCCT 680
QY 784 CCGGCTGCCCAACCAAGTGTCTCTGCGAGCTGCAAGAGGGCCAGATCTACTGCGGCC 843
DB 681 CCGGCTGCCCAACCAAGTGTCTCTGCGAGCTGCAAGAGGGCCAGATCTACTGCGGCC 740
QY 844 TCACAACTGCGCCGAAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 903
DB 741 TCACAACTGCGCCGAAACAGGCTGCCAGCACCCCTCCCGCTGCCAGACTCTCTGCTGCC 800
QY 904 AAGCTCTGCAAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 963
DB 801 AAGCTCTGCAAGATGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 860
QY 964 ATGGGTGAGACATCTCTCAGGATCCAATGTTTCAAGTGTCTGGGAGAAAGAGAGCCGG 1023
DB 861 ATGGGTGAGACATCTCTCAGGATCCAATGTTTCAAGTGTCTGGGAGAAAGAGAGCCGG 920
QY 1024 GCACCCAGCCCACTTGGGCTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTTCAGAC 1083
DB 921 GCACCCAGCCCACTTGGGCTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTTCAGAC 980
QY 1084 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143
DB 981 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
QY 1144 GTGTGATGGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203

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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
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; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
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; PRIOR APPLICATION NUMBER: 60/101476
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; PRIOR APPLICATION NUMBER: 60/102687
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; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
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; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
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; PRIOR APPLICATION NUMBER: 60/103314
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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
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; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
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; PRIOR FILING DATE: 1998-10-08

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; PRIOR APPLICATION NUMBER: 60/103679
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
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; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
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; PRIOR APPLICATION NUMBER: 60/105000
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; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
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; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
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; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
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; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
;
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
;
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
;
; PRIOR FILING DATE: 1998-10-28

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY	424	TTGGGCTGGAGCCTCTCGGACATAACATGGCACTGGTGGTTTCCAGAGCCGACACATGT	483
DB	321	TGGGACTCGCGTCTGTGGTTCCCTCGACTCCAGCTCCAGAGCCGACACATGT	380
QY	484	TCTGCCTTTTCATGGGAAGAGATATCCCCCGGGGAGAGCTGGGACCCCTACTTGGAGC	543
DB	381	TCTGCCTTTTCATGGGAAGAGATATCCCCCGGGGAGAGCTGGGACCCCTACTTGGAGC	440
QY	544	CACAAGGCTGATGTACTGCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGT	603
DB	441	CACAAGGCTGATGTACTGCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGT	500
QY	604	ACGCGCTCCACTGTCCGCTGTCCACTGCGCCCGAGCTGTGACGGAGCCACAGCAATGCT	663
DB	501	ACGCGCTCCACTGTCCGCTGTCCACTGCGCCCGAGCTGTGACGGAGCCACAGCAATGCT	560
QY	664	GTCCGAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCGCCACCAAGTCTGCC	723
DB	561	GTCCGAAGTGTGGAACTCACACTCCCTCTGGACTCCGGGCCGCCACCAAGTCTGCC	620
QY	724	AGCAAAAGGACCATGTAACAACAGGAGATTTTCAAGTGCCCATGAGCTGTTCCT	783
DB	621	AGCAAAAGGACCATGTAACAACAGGAGATTTTCAAGTGCCCATGAGCTGTTCCT	680
QY	784	CCGCGCTGCCCAAGCAGTGTCTCTGAGCTGACAGAGGGCCAGATCTACTCGGACC	843
DB	681	CCGCGCTGCCCAAGCAGTGTCTCTGAGCTGACAGAGGGCCAGATCTACTCGGACC	740
QY	844	TCACAACTGCCCGGAACAGGCTGCCAGACCCCTCCGCTGCCAGATCTCTGCTGCC	903
DB	741	TCACAACTGCCCGGAACAGGCTGCCAGACCCCTCCGCTGCCAGATCTCTGCTGCC	800
QY	904	AAGCTGCAAGATGAGGCAAGTGAAGATCGATGAAGAGGACATGTGAGTGTCTGCC	963
DB	801	AAGCTGCAAGATGAGGCAAGTGAAGATCGATGAAGAGGACATGTGAGTGTCTGCC	860
QY	964	ATGGGTGAGACATCTCTCAGGATCCATGTTCAGTGTGCTGGAGAAAGAGGCGCGG	1023

Db 861 ATGGGGTGAGACATCCTCAGGATCCATGTTTCCAGTGATGCTGGGAGAAAAGAGAGCCCGG 920
QY 1024 GCACCCAGCCCCCACTGGCTCAGCGCCCTCTGAGTTCATCCTCGCACATTCAGAC 1083
Db 921 GCACCCAGCCCCCACTGGCTCAGCGCCCTCTGAGTTCATCCTCGCACATTCAGAC 980
2Y 1084 CCAAGGAGAGGCGAGCACTCTGAGATCGTCTGAAGGAGAAACATAGAAAGCCT 1143
Db 981 CCAAGGAGAGGCGAGCACTCTGAGATCGTCTGAAGGAGAAACATAGAAAGCCT 1040
2Y 1144 GTGTGCATGCGCGGAGAGAGCTATCCCAAGGAGAGGTGTGGCAACCGGCTCTCGTGCT 1203
Db 1041 GTGTGCATGCGCGGAGAGAGCTATCCCAAGGAGAGGTGTGGCAACCGGCTCTCGTGCT 1100
QY 1204 TCGGCCCCCTTGGCTTGCATCTCTATGCACTCTGAGGATGGCGGCGAGGATGCCAGCGTG 1263
Db 1101 TCGGCCCCCTTGGCTTGCATCTCTATGCACTCTGAGGATGGCGGCGAGGATGCCAGCGTG 1160
QY 1264 TGACCTGTCCCAAGGATACCCCTGCGTCCACCCGAGAAAGTGGCTGGGAGAGTGTGCA 1323
Db 1161 TGACCTGTCCCAAGGATACCCCTGCGTCCACCCGAGAAAGTGGCTGGGAGAGTGTGCA 1220
QY 1324 AGATTGCCAGAGAGCAAGAGAGAGAGCTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1383
Db 1221 AGATTGCCAGAGAGCAAGAGAGAGAGAGCTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1280
QY 1384 CCAAGGACCGGGCGGGGTCTCTGTCACACATCGGTATCCCAAGGCCAGCAACCTGC 1443
Db 1281 CCAAGGACCGGGCGGGGTCTCTGTCACACATCGGTATCCCAAGGCCAGCAACCTGC 1340
QY 1444 GTGCGTTTGGCTTGGAAACACGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1503
Db 1341 GTGCGTTTGGCTTGGAAACACGAGGCTCGGACTTGGTGAGATCTACCTCTGGAAGCTGG 1400
QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
QY 1564 AGAATCTTCCACTTGACTCAGATCAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1623
Db 1461 AGAATCTTCCACTTGACTCAGATCAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1520
QY 1624 CAGCACTTCCGACTGCTCGCTGGCCCCCAGAAAGTCACTGGAACGTCTTCTTAGCCAG 1683
Db 1521 CAGCACTTCCGACTGCTCGCTGGCCCCCAGAAAGTCACTGGAACGTCTTCTTAGCCAG 1580
QY 1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGCAAGAGTGAAGCAAGTGAAGCAAGTGAAGCAAGT 1743
Db 1581 ACCCTGGAGCTGAAGGTCAAGGCTCAGCAAGAGTGAAGCAAGTGAAGCAAGTGAAGCAAGT 1640
QY 1744 AACAGTTCAGATATGAGCTGTATTAATTTGTTTATATATATTAATTAATTAAGAAAGTTG 1803
Db 1641 AACAGTTCAGATATGAGCTGTATTAATTTGTTTATATATATTAATTAATTAAGAAAGTTG 1700
QY 1804 CATAACCATCAAAA 1817
Db 1701 CATTACCCCTCAAAA 1714

RESULT 10

US-10-187-749-281

; Sequence 281, Application US/10187749

; Publication No. US2003015936A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Collin K.

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCCTCTGGGACTAAATGACATGCTGGTTCGAGGTTTCCAGGCCAGACATGT 483
Db 321 TGGGACTGGCGCTGCTCTGGTTCGCCCTGAGCTCCACGCTCGAGCCGCCAGACATGT 380
QY 484 TCTGCCTTTTCCATGGAAAGAGATCTCCCCCGGCGAGAGCTGGCAACCTTCTGGAGC 543
Db 381 TCTGCCTTTTCCATGGAAAGAGATCTCCCCCGGCGAGAGCTGGCAACCTTCTGGAGC 440
QY 544 CACAAGGCTGATGTACTGCTGCGCTGTACTCTCAGAGGGCGGCCCATGTGAGTTGTT 603
Db 441 CACAAGGCTGATGTACTGCTGCGCTGTACTCTCAGAGGGCGGCCCATGTGAGTTGTT 500
QY 604 ACCGCTCCACTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 501 ACCGCTCCACTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAACTCTACACTCCCTTGGACTCCGAGCCGCCAGCAAGTCTGCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCTACACTCCCTTGGACTCCGAGCCGCCAGCAAGTCTGCTGCC 620
QY 724 AGCAACAACCGGACCATGTATACCAACAAGAGAGATCTTTCAGTGCCTCCATGAGTGTTCCT 783
Db 621 AGCAACAACCGGACCATGTATACCAACAAGAGAGATCTTTCAGTGCCTCCATGAGTGTTCCT 680
QY 784 CCGGCTGCCCCCAACCAAGTGTGCTCTCTGCAAGTGTGCAAGGGCCAGATCTTCTAGTGGGCC 843
Db 681 CCGGCTGCCCCCAACCAAGTGTGCTCTCTGCAAGTGTGCAAGGGCCAGATCTTCTAGTGGGCC 740
QY 844 TCACAACCTGCCCCGAGAACAGAGCTGCGCCAGCACCTCTCCGCTGCGCACACTCTCTGCTGCC 903
Db 741 TCACAACCTGCCCCGAGAACAGAGCTGCGCCAGCACCTCTCCGCTGCGCACACTCTCTGCTGCC 800
QY 904 AAGCTGCAAAAGATAGGCGAAGTGAAGCATCGATGAAGAGAGAGTGTGAGTGTGAGTGTGCTCC 963

801 AAGCCTGCAAGATGAGCAAGTGAAGATCGGATGAAGAGGACAGTGTGCGTCTCC 860
964 ATGGGTGAGACATCTCCAGGATCCATGTTTCATGATGATGCTGGGAAAGAGAGCCCGG 1023
861 ATGGGTGAGACATCTCCAGGATCCATGTTTCATGATGATGCTGGGAAAGAGAGCCCGG 920
1024 GCACCCAGCCCGCCAGTGGCTCAGCGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 1083
921 GCACCCAGCCCGCCAGTGGCTCAGCGCCCTCTGAGCTTCACTCCCTGCCACTTCAGAC 980
1084 CMAGGGAGCGAGGAGCAGCACAACCTGTCAAGATGCTCTGAAGGAGAAACATGAAGACCT 1143
981 CCAAGGGAGCAGGAGCAGCACAACCTGTCAAGATGCTCTGAAGGAGAAACATGAAGACCT 1040
1144 GTGTGATGCGGGAGAACGACTACTCCCAAGCGGGAGGTGTGGCACCCCGCCCTTCGTCCT 1203
1041 GTGTGATGCGGGAGAACGACTACTCCCAAGCGGGAGGTGTGGCACCCCGCCCTTCGTCCT 1100
1204 TCGGCCCTTGCCTGCTATCTATGACCTGTGAGGATGGCCCGCAGGACTGCCAGGTG 1263
1101 TCGGCCCTTGCCTGCTATCTATGACCTGTGAGGATGGCCCGCAGGACTGCCAGGTG 1160
1264 TGACCTGTCCACCGAGTACCTCTGCGCTCACCOCGAGAAAGTGGCTGGGAAGTGTGCA 1323
1161 TGACCTGTCCACCGAGTACCTCTGCGCTCACCOCGAGAAAGTGGCTGGGAAGTGTGCA 1220
1324 AGATTGGCCAGAGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAAGGTGTC 1383
1221 AGATTGGCCAGAGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAAGGTGTC 1280
1384 CCAAGGCACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCGCAGACACCTGC 1443
1281 CCAAGGCACCGGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCGCAGACACCTGC 1340
1444 GTGCTTTTCCCTGGACACAGGAGCTCTGAGTGTGGAGATCTACCTCTGGAAGCTGG 1503
1341 GTGCTTTTCCCTGGACACAGGAGCTCTGAGTGTGGAGATCTACCTCTGGAAGCTGG 1400
1504 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACTGTGCCCGCAGGCCACACAGCC 1563
1401 TAAAGATGAGAACTGAGGCTCAGAGAGTGAAGTACTGTGCCCGCAGGCCACACAGCC 1460
1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCCA 1623
1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGCCA 1520
1624 CAGCACTTCCGACTGCTGCTGCGCCCGCCACGAGGTCACTGGAACGCTTCTAGCCCGAG 1683
1521 CAGCACTTCCGACTGCTGCTGCGCCCGCCACGAGGTCACTGGAACGCTTCTAGCCCGAG 1580
1684 ACCCTGGAGCTGAAGGTCAAGGCGAGTCCAGCAAAAGTGAAGCAAGACTTAACAAAGCT 1743
1581 ACCCTGGAGCTGAAGGTCAAGGCGAGTCCAGCAAAAGTGAAGCAAGACTTAACAAAGCT 1640
1744 AACAGTTGAGATGAGCTGTATAATTTGTTATTATATATAATAATAAAGAGTTG 1803
1641 AACAGTTGAGATGAGCTGTATAATTTGTTATTATATATAATAATAAAGAGTTG 1700
1804 CATTAACCTCAAAA 1817
1701 CATTAACCTCAAAA 1714

RESULT 11
US-10-194-457-281
Sequence 281, Application US/10194457
Publication No. US2003015307A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P343081C296
CURRENT APPLICATION NUMBER: US/10/194,457
PRIOR FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-194-457-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCTCTCTGGGACTAAATGCGACTGTGGTGGTTTCCAGGCCCGCAGACATGT 483
DB 321 TGGGACTCGCGTGTCTGTGTTCCCTCCGACTCCACGCTCGAGGCCCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGTGGCACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGTGGCACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGTACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
DB 441 CACAAGGCTGTACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 604 ACCGCTTCCACTGTCCGCTGTCCACTGCCCGCCAGCTGTGACGAGGCCACAGCAATGCT 663
DB 501 ACCGCTTCCACTGTCCGCTGTCCACTGCCCGCCAGCTGTGACGAGGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGAAGTCTCCGCGCCCGCCCAAGAGTCTGCC 723
DB 561 GTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGAAGTCTCCGCGCCCGCCCAAGAGTCTGCC 620
QY 724 AGCACAACGGGACCATGTACCAACGAGAGATCTTCAGTGGCCCTCATGAGTGTTCCTCCT 783
DB 621 AGCACAACGGGACCATGTACCAACGAGAGATCTTCAGTGGCCCTCATGAGTGTTCCTCCT 680
QY 784 CCGGCTTCCGACCAAGCTGTGCTCTGCTGAGCTGCAAGAGGCCGAGTCTACTCGGCC 843
DB 681 CCGGCTTCCGACCAAGCTGTGCTCTGCTGAGCTGCAAGAGGCCGAGTCTACTCGGCC 740
QY 844 TCACAACTGCCCCGACCAAGCTGAGGCTGCCAGACCCCTCCGCTGCCAGCTCTCCTGCTGCC 903

741 TCACAACTGCCCCGACCAAGGTGCCAGACCCCTCCCACTGCCAGACTCCTGCTGCC 800
742
904 AAGCTTGCAAGATGAGGAGTGCACATCGATGAGAGGACAGTGTGAGTGCCTCC 963
905
801 ARCCCTGCAAGATGAGCAAGTGAAGATCGATGAAGAGGACAGTGTGAGTGCCTCC 860
802
964 ATGGGTGAGACATCCTCAGATGCAATGTTCCAGTGTGCTGGGAGAGAGAGCCCGG 1023
965
861 ATGGGTGAGACATCCTCAGATGCAATGTTCCAGTGTGCTGGGAGAGAGAGCCCGG 920
862
1024 GCACCCAGCCCCCACTGGCTCAGGCCCCCTCTGAGTTTCACTCCCTGSCCACTTCAGAC 1083
1025
921 GCACCCAGCCCCCACTGGCTCAGGCCCCCTCTGAGTTTCACTCCCTGSCCACTTCAGAC 980
922
1084 CCAAGGAGCAGCAGACCACTGTCAAGATGCTCTCAAGGAGAGAACATAGAAGGCT 1143
1085
981 CCAAGGAGCAGCAGACCACTGTCAAGATGCTCTCAAGGAGAGAACATAGAAGGCT 1040
982
1144 GTGTGCAATGGCGGAGAGCACTCTCCACAGGAGAGTGTGGACCCGCGCTTCCGTGCT 1203
1145
1041 GTGTGCAATGGCGGAGAGCACTCTCCACAGGAGAGTGTGGACCCGCGCTTCCGTGCT 1100
1042
1204 TCGGCCCCCTGCTGCTGCTTCTTCACTGTGAGATGGCGGAGGAGTGTGGAGGCTG 1263
1205
1101 TCGGCCCCCTGCTGCTGCTTCTTCACTGTGAGATGGCGGAGGAGTGTGGAGGCTG 1160
1102
1264 TGACCTGTCCCAACGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
1265
1161 TGACCTGTCCCAACGAGTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1220
1162
1324 AGATTTCCTCAGAGGAG 1383
1325
1221 AGATTTCCTCAGAGGAG 1280
1222
1384 CCAAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1443
1385
1281 CCAAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1340
1282
1444 GTGCGTTTGGCTTGGAAACAGAGGCTTGGAGTGTGGAGATCTACTCTGGAAGCTGG 1503
1445
1341 GTGCGTTTGGCTTGGAAACAGAGGCTTGGAGTGTGGAGATCTACTCTGGAAGCTGG 1400
1342
1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGAGTGAAGTACTGGCCCAAGGCCACAGCC 1563
1505
1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGAGTGAAGTACTGGCCCAAGGCCACAGCC 1460
1402
1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAG 1623
1565
1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAG 1520
1462
1624 CAGCACTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683
1625
1521 CAGCACTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
1522
1684 ACCCTGGAGCTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
1685
1581 ACCCTGGAGCTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
1582
1744 AACAGTTCAGATGAGTGTGATATTTGTTGTTTATATATATATATATATATATATAT 1803
1745
1641 AACAGTTCAGATGAGTGTGATATTTGTTGTTTATATATATATATATATATATATAT 1700
1642
1804 CATACACATCAAA 1817
1805
1701 CATACACCTCAAA 1714
1702

RESULT 12

US-10-184-642-281
; Sequence 281, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P430R1C194
CURRENT APPLICATION NUMBER: US/10/184,642
CURRENT FILING DATE: 2002-06-27
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
US-10-184-642-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTGGAGCTCTCGGACTAACTGACACTGGTGGTTCGAGGCCAGACATGT 483
DB 321 TGGGACTCGGCTGTCTGTTCCCTCGACTCCAGCTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCTTTTCCATGGGAGAGATCTCCCTCGGCGAGAGCTGACACCTCTTGGAGC 543
DB 381 TCTGCTTTTCCATGGGAGAGATCTCCCTCGGCGAGAGCTGGCACTCTTGGAGC 440
QY 544 CACAAGGCTGTGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
DB 441 CACAAGGCTGTGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
QY 604 ACCGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
DB 501 ACCGCTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
DB 561 GTCCCAAGTGTGGAACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 724 AGCAACAAGGAGCCATGTATCCAAACAAGGAGATCTTCAGTGCCCATGAGTGTGCTGCT 783
DB 621 AGCAACAAGGAGCCATGTATCCAAACAAGGAGATCTTCAGTGCCCATGAGTGTGCTGCT 680
QY 784 CCGGCTGCCCAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 681 CCGGCTGCCCAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 844 TCACAACTGCTCCGGAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
DB 741 TCACAACTGCTCCGGAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 904 AAGCTTCAAGATGAGGCAAGTGAAGCATCGATGAAGAGAGAGTGTGAGTGTGCTGCTGCT 963
DB 801 AAGCTTCAAGATGAGGCAAGTGAAGCATCGATGAAGAGAGAGTGTGAGTGTGCTGCTGCT 860
QY 964 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGGCCCGG 1023
DB 861 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGGCCCGG 920
QY 1024 GCACCCAGGCCCCCACTGGCTCAGGCCCCCTCTGAGTCTTCATCCCTGCCACTTCAGAC 1083
DB 921 GCACCCAGGCCCCCACTGGCTCAGGCCCCCTCTGAGTCTTCATCCCTGCCACTTCAGAC 980
QY 1084 CCAAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143

981 CCAAGGAGCAGGAGGAGCAACATGTCAGATGCTCTGAAGGAGAGAAACATAGAAAGCCT 1040
1144 GTGTGCATGGCGGAGAGACATCTCCACAGGGAGGTGTGGCACCCGGCCTTCGTGCCT 1203
1041 GTGTGCATGGCGGAGAGACATCTCCACAGGGAGGTGTGGCACCCGGCCTTCGTGCCT 1100
1204 TCGGCCCTTCGCTGATCTATGACATCTGTAGGATGCGCCAGGACTGCCAGCGTG 1263
1101 TCGGCCCTTCGCTGATCTATGACATCTGTAGGATGCGCCAGGACTGCCAGCGTG 1160
1264 TGACCTGTCACAGGATGACCTGCGCTGACCCCGAGAGAGTGGTGGAGTGCAGCA 1323
1161 TGACCTGTCACAGGATGACCTGCGCTGACCCCGAGAGAGTGGTGGAGTGCAGCA 1220
1324 AGATTGGCCAGAGGAGCAAGAGAGACCTGTGGCACAAGTGAATGATCTTACAGAGTGC 1383
1221 AGATTGGCCAGAGGAGCAAGAGAGACCTGTGGCACAAGTGAATGATCTTACAGAGTGC 1280
1384 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCCAAGCCCGAGACAACTGC 1443
1281 CCAAGGACACCGGGCGGGTCTCTGTCACACATCGGTATCCCCAAGCCCGAGACAACTGC 1340
1444 GTGCTTTGCTTGGGAGACAGAGGCTCTGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1503
1341 GTGCTTTGCTTGGGAGACAGAGGCTCTGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1400
1504 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAATCTGCTGGCCCGAGGACACACAGCC 1563
1401 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAATCTGCTGGCCCGAGGACACACAGCC 1460
1564 AGAATCTTCACTTGAATCAGATCAAGAAAGTCAAGGAGCAAGACTTCCAGAAAGAGCA 1623
1461 AGAATCTTCACTTGAATCAGATCAAGAAAGTCAAGGAGCAAGACTTCCAGAAAGAGCA 1520
1624 CAGACTTCCAGACTGCTCGTGGCCCGCCACAGAGTCACTGGAAAGCTTCTCTAGGCCAG 1683
1521 CAGCACTTCGAGCTGCTGCTGGCCCGCCACAGAGTCACTGGAAAGCTTCTCTAGGCCAG 1580
1684 ACCCTGGAGCTGAGGCTCAGGCGAGTCCAGCAAGTGAACCAAGGACATCAAGAGACT 1743
1581 ACCCTGGAGCTGAGGCTCAGGCGAGTCCAGCAAGTGAACCAAGGACATCAAGAGACT 1640
1744 AACAGTGCAGATATGAGCTGTAAATGCTGTTATTATATATTAATAATAAGAGTTG 1803
1641 AACAGTGCAGATATGAGCTGTAAATGCTGTTATTATATATTAATAATAAGAGTTG 1700
1804 CATAACCATCAAAA 1817
1701 CATTACCCCTCAAAA 1714

RESULT 13
US-10-196-747-281
Sequence 281, Application US/10196747
Publication No. US20030162250A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P430R1C346
CURRENT APPLICATION NUMBER: US/10/196,747
CURRENT FILING DATE: 2002-07-16
Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-747-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
424 TTGGGCTGGAGCTCTCGGACTAAACATGGCACTGGTGGCTTTGCCAGGCCCGACAGATGT 483
321 TGGGACTCGCGTGTCTGTGTTCCCTCGACTCCAGCTCCAGGCCCGCCGACAGATGT 380
484 TCTGCTTTTCCATGGGAAGATATCTCCCGGGAGAGAGTGGCACTTCTGGAGC 543
381 TCTGCTTTTCCATGGGAAGATATCTCCCGGGAGAGAGTGGCACTTCTGGAGC 440
544 CACAAGGCTGTATGTATCTGCTGCTGTACCTGTCTAGAGGGCGCCCATGTGAGTTGTT 603
441 CACAAGGCTGTATGTATCTGCTGCTGTACCTGTCTAGAGGGCGCCCATGTGAGTTGTT 500
604 ACCGCTTCCACTGTCCGCTGTCCACTGCCCCCAGCTGTGA CGGAGCCACAGCAATGCT 663
501 ACCGCTTCCACTGTCCGCTGTCCACTGCCCCCAGCTGTGA CGGAGCCACAGCAATGCT 560
664 GTCCCAAGTGTGTGAAGCTCA CACTCCCTCTGAGCTTCGCGGCCCGCCACCAAGTCTCTGCC 723
561 GTCCCAAGTGTGTGAAGCTCA CACTCCCTCTGAGCTTCGCGGCCCGCCACCAAGTCTCTGCC 620
724 AGCAAAACGGGACCATGTGTACCAACCGGAGAGATCTTCA GTGCTCCATGAGCTGTCCCT 783
621 AGCAAAACGGGACCATGTGTACCAACCGGAGAGATCTTCA GTGCTCCATGAGCTGTCCCT 680
784 CCGGCTTCCGCAAAACAGTGTCTCTGCTGAGCTGCA CAGAGGGCCAGATCTACTCGCGCC 843
681 CCGGCTTCCGCAAAACAGTGTCTCTGCTGAGCTGCA CAGAGGGCCAGATCTACTCGCGCC 740
844 TCACACTGCTCCGCAACAGGCTGCGCCAGCACCCCTCCGCTGCCAGACTCTCTCTGCC 903
741 TCACACTGCTCCGCAACAGGCTGCGCCAGCACCCCTCCGCTGCCAGACTCTCTCTGCC 800
904 AACCTGCAAGATGAGGCAAGTGAACAATCGATGGAAGAGGACATGTGTGCA GTCGCTCC 963
801 AACCTGCAAGATGAGGCAAGTGAACAATCGATGGAAGAGGACATGTGTGCA GTCGCTCC 860
964 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 1023
861 ATGGGCTGAGACATCTCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAGAGAGCCCGG 920
1024 GCACCCCGCCCGCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
921 GCACCCCGCCCGCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
1084 CCAAGGAGCAGGACAGCAACAATCTGCAAGTCTCTGAGAGGAGAAACATAGAAAGCT 1143
981 CCAAGGAGCAGGACAGCAACAATCTGCAAGTCTCTGAGAGGAGAAACATAGAAAGCT 1040
1144 GTGTGATGCGGGAGAGACATCTCTCCACCGGAGAGGTGTGGCA CCGCGCTTCGTGCT 1203
1041 GTGTGATGCGGGAGAGACATCTCTCCACCGGAGAGGTGTGGCA CCGCGCTTCGTGCT 1100
1204 TCGGCCCTTTCGCTGTATCTCTATGACATCTGTGAGGATGGCCCGCCAGGACTGCCAGGTG 1263
1101 TCGGCCCTTTCGCTGTATCTCTATGACATCTGTGAGGATGGCCCGCCAGGACTGCCAGGTG 1160
1264 TGACCTGTCACAGGATGACCTGCGCTGACCCCGAGAGAGTGGTGGAGTGCAGCA 1323
1161 TGACCTGTCACAGGATGACCTGCGCTGACCCCGAGAGAGTGGTGGAGTGCAGCA 1220
1324 AGATTGGCCAGAGGAGCAAGAGAGACCTGTGGCACAAGTGAATGATCTTACAGAGTGC 1383

Db 1221 AGATTTGCCAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTTACCAGGTGC 1280
QY 1384 CCAAGGCACCGGGCGGGTCTCTCTCCACACATCGGTATCCCAAGCCAGACACCTGC 1443
Db 1281 CCAAGGCACCGGGCGGGTCTCTCTCCACACATCGGTATCCCAAGCCAGACACCTGC 1340
QY 1444 GTGCTTTGCCCTGGAAACACAGAGCCCTCGACTTGGTGGAGATCTACTCTTGGAGCTGG 1503
Db 1341 GTGCTTTGCCCTGGAAACACAGAGCCCTCGACTTGGTGGAGATCTACTCTTGGAGCTGG 1400
QY 1504 TAAAGATGAGGAATCTGAGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAATCTGAGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
QY 1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGAAAGCAAGACTTCCAGAAAGAGCA 1623
Db 1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGAAAGCAAGACTTCCAGAAAGAGCA 1520
QY 1624 CAGCACTTCCGACTCGCTGGCGCCCGCCAGAGGTCTACTGGAGCTTCTTCCAGCCAG 1683
Db 1521 CAGCACTTCCGACTCGCTGGCGCCCGCCAGAGGTCTACTGGAGCTTCTTCCAGCCAG 1580
QY 1684 ACCCTGAGCTGAAGTCAAGGCTCAGAGAGGTGCAAGAAAGTGAACAAGAGACT 1743
Db 1581 ACCCTGAGCTGAAGTCAAGGCTCAGAGAGGTGCAAGAAAGTGAACAAGAGACT 1640
QY 1744 AACAGTTGAGATATGAGCTGTATAATTTGTTATTATATTAATAAATAAGAGTTG 1803
Db 1641 AACAGTTGAGATATGAGCTGTATAATTTGTTATTATATTAATAAATAAGAGTTG 1700
QY 1804 CATACCATCAAA 1817
Db 1701 CATTACCTCAAA 1714

RESULT 14

US-10-015-392A-141
; Sequence 141, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-392A-141
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTTGGAGCTCTCTGGGACTAAATGSCACTGGTGGTTTGCAGGCCCGACATGT 483
Db 321 TGGGACTTGGCGCTGTCTTGTCTCCCTCGACTCCCAAGCTCGAGCCGCGCCAGATGT 380
QY 484 TCTGCTTTTCCATGGGAAGAGATATCTCCCGGCGAGAGCTGGGACCCCTACTTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAAGAGATATCTCCCGGCGAGAGCTGGGACCCCTACTTGGAGC 440
QY 544 CACAAGGCCCTGATGTACTGCTGCGCTGTACCTGTCTCAGAGGGCGCCCATGTGAGTTGT 603
Db 441 CACAAGGCCCTGATGTACTGCTGCGCTGTACCTGTCTCAGAGGGCGCCCATGTGAGTTGT 500
QY 604 ACCGCTTCACTTCCGCTGTCCACTGGCCCCAGCTGTGACGGAGCCACACAATGT 663
Db 501 ACCGCTTCACTTCCGCTGTCCACTGGCCCCAGCTGTGACGGAGCCACACAATGT 560
QY 664 GTCCCAAGTGTGGAACTCAGACTCCCTTGGACTCCGGGCCCCACCAATCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCAGACTCCCTTGGACTCCGGGCCCCACCAATCTCTGCC 620
QY 724 AGCAACAAGGACATGTATCAACAAGAGAGATCTTCAAGTGGCCATGAGCTTCCCT 783
Db 621 AGCAACAAGGACATGTATCAACAAGAGAGATCTTCAAGTGGCCATGAGCTTCCCT 680
QY 784 CCGCTTCCGCCCCAACCAAGTGTCTCTGCAAGTGCACAGAGGGCCAGATCTACTCGGCC 843
Db 681 CCGCTTCCGCCCCAACCAAGTGTCTCTGCAAGTGCACAGAGGGCCAGATCTACTCGGCC 740
QY 844 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCCTGCCAGACTCTCTGTGCC 903
Db 741 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCCTGCCAGACTCTCTGTGCC 800
QY 904 AAGCTCTCAAGATGAGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTGGCTCC 963
Db 801 AAGCTCTCAAGATGAGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTGGCTCC 860
QY 964 ATGGGGTGACATCTCTCAGATCCATGTTCAGTGTGAGAGAAAAGAGGCCCG 1023
Db 861 ATGGGGTGACATCTCTCAGATCCATGTTCAGTGTGAGAGAAAAGAGGCCCG 920
QY 1024 GCACCCCGAGCCCCCACTGGCTCAGCGCCCCCTCTCAGCTTCATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCCGAGCCCCCACTGGCTCAGCGCCCCCTCTCAGCTTCATCCCTCGCCACTTCAGAC 980
QY 1084 CCAAGGAGCAGGACGACCAACTCTCAAGATGTCTGAAGGAAACAAATAAGAAAGCT 1143
Db 981 CCAAGGAGCAGGACGACCAACTCTCAAGATGTCTGAAGGAAACAAATAAGAAAGCT 1040
QY 1144 GTGTGCAATGGCGGAGAGCTACTTCCCAAGGAGGTGTGGACCCCGCTTCCGTGCT 1203
Db 1041 GTGTGCAATGGCGGAGAGCTACTTCCCAAGGAGGTGTGGACCCCGCTTCCGTGCT 1100
QY 1204 TCGGCCCCCTTGGCTTCATCTTATGCACTGTGAGGATGGCGCCGACGAGATGCCAGCTG 1263
Db 1101 TCGGCCCCCTTGGCTTCATCTTATGCACTGTGAGGATGGCGCCGACGAGATGCCAGCTG 1160

1264 TGACCTGTCCACCGAGTACCCCTGCGCTGACCCCGAGAAAGTGGCTGGAAAGTCTGCA 1323
1161 TGACCTGTCCACCGAGTACCCCTGCGCTGACCCCGAGAAAGTGGCTGGAAAGTCTGCA 1220
1324 AGATTTGCCCGAGAGCAAAAGCAGACAGCCCTGGCCACAGTGAGATCACTTACCAAGGTGC 1383
1221 AGATTTGCCCGAGAGCAAAAGCAGACAGCCCTGGCCACAGTGAGATCACTTACCAAGGTGC 1280
1384 CCAAGGACCCGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCAAGCAACCTGC 1443
1281 CCAAGGACCCGGCGGGTCTCTGTCACACATCGGTATCCCAAGCCCAAGCAACCTGC 1340
1444 GTGCTTTGCCCTGGACACAGAGCTCGAGCTGGTGGAGATCTACTCTTGGAAAGCTGG 1503
1341 GTGCTTTGCCCTGGACACAGAGCTCGAGCTGGTGGAGATCTACTCTTGGAAAGCTGG 1400
1504 TAAAGATGAGAAACTGAGCTCAGAGAGTGAGTACCTGGCCCAAGGCCACACAGCC 1563
1401 TAAAGATGAGAAACTGAGCTCAGAGAGTGAGTACCTGGCCCAAGGCCACACAGCC 1460
1564 AGAATCTTCCACTTGATTCAGATCAAGAAAGTCAAGAAAGCAAGACTTCCAGAAAGGCCA 1623
1461 AGAATCTTCCACTTGATTCAGATCAAGAAAGTCAAGAAAGCAAGACTTCCAGAAAGGCCA 1520
1624 CAGCACTTCGAGCTGCTGCTGCGCCCGCCAGAGGTCACTGGAAAGTCTTCTAGCCCGAG 1683
1521 CAGCACTTCGAGCTGCTGCTGCGCCCGCCAGAGGTCACTGGAAAGTCTTCTAGCCCGAG 1580
1684 ACCTGGAGCTGAAGGTGACCGGCTCCAGCAAAAGTCAAGCAAAAGTCAAGCAAAAGACCT 1743
1581 ACCTGGAGCTGAAGGTGACCGGCTCCAGCAAAAGTCAAGCAAAAGTCAAGCAAAAGACCT 1640
1744 AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATATATTAATAAATAAGAAAGTTG 1803
1641 AACAGTTGCAGATATGAGCTGTATATTTGTTTATTATATATTAATAAATAAGAAAGTTG 1700
1804 CATAACCAATCAAAA 1817
1701 CATACCTTCAAAA 1714

ESULT 15
US-10-017-253A-141
Sequence 141, Application US/10017253A
Publication No. US20030166055A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC62
CURRENT APPLICATION NUMBER: US/10/017,253A
PRIOR FILING DATE: 2001-12-13
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 141
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-253A-141
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGCTGGAGCTCTCGGACTTAATCGCACTGCTGGTTTGCAGGCCCAAGCATGT 483
DB 321 TGGGACTCGCGTGTCTGTGTTCCCTCGGACTCCACGCTCGAGGCCCGCCAGACATGT 380
QY 484 TCTGCTTTTTCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCAACCTTACTTTGGAGC 543
DB 381 TCTGCTTTTTCATGGGAAGAGATATCTCCCGCGGAGAGCTGGCAACCTTACTTTGGAGC 440
QY 544 CACAAGGCTGTATGTACTGCTGCTGTACTGCTGTACCTGCTCAGAGGGCGCCATGTAGTGTGT 603
DB 441 CACAAGGCTGTATGTACTGCTGCTGTACTGCTGTACCTGCTCAGAGGGCGCCATGTAGTGTGT 500
QY 604 ACCGCTTCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
DB 501 ACCGCTTCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCCAAGTGTGGAACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
DB 561 GTCCCAAGTGTGGAACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
QY 724 AGCAACAACGGGACCATGTACCAACAGGAGAGATCTTTCAGTGGCCCATGAGTGTGCTGCT 783
DB 621 AGCAACAACGGGACCATGTACCAACAGGAGAGATCTTTCAGTGGCCCATGAGTGTGCTGCT 680
QY 784 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 681 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 844 TCACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
DB 741 TCACAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 904 AAGCTTGCAGAAAGTGGGCAAGTGAAGCAATCGATGAAGAGGACAGTGTGCAAGTGTGCTGCT 963
DB 801 AAGCTTGCAGAAAGTGGGCAAGTGAAGCAATCGATGAAGAGGACAGTGTGCAAGTGTGCTGCT 860
QY 964 ATGGGTGAGACATCTCTCAGGATCTCATGTTCCAGTGTGCTGCGAGAAAGAGAGGCCCGG 1023
DB 861 ATGGGTGAGACATCTCTCAGGATCTCATGTTCCAGTGTGCTGCGAGAAAGAGAGGCCCGG 920
QY 1024 GACACCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1083
DB 921 GACACCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 980
QY 1084 CCAAGGAGCAGGAGCAGCAACCTGTCTAAGATGTCTGCTGAAGAGGAGAAACATAGAAAGCCT 1143
DB 981 CCAAGGAGCAGGAGCAGCAACCTGTCTAAGATGTCTGCTGAAGAGGAGAAACATAGAAAGCCT 1040

1384 CCAAGCACCGGGCGGGTCTCTGTCACACATCGATATCCCAAGCCCAACACGACCTGC 1443
1281 CCAAGGCAACCGGGCGGGTCTCTGTCACACATCGATATCCCAAGCCCAACACGACCTGC 1340
1444 GTGCGTTTGGCCCTCGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTCGAAGCTGG 1503
1341 GTGCGTTTGGCCCTCGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTCGAAGCTGG 1400
1504 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCCAACAGACC 1563
1401 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCCAACAGACC 1460
1564 AGAATCTTCCACTTGACCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1623
1461 AGAATCTTCCACTTGACCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1520
1624 CAGCACTTCCGACTGCTCGCTGGCCGCCCAAGAGGTCACTGGAAAGTCTTCTTCTAGGCCAG 1683
1521 CAGCACTTCCGACTGCTCGCTGGCCGCCCAAGAGGTCACTGGAAAGTCTTCTTCTAGGCCAG 1580
1684 ACCCTGGAGCTGAAGGTCAGGGCCAGTCCAGACAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGT 1743
1581 ACCCTGGAGCTGAAGGTCAGGGCCAGTCCAGACAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGT 1640
1744 AAGAGTTCAGATATGAGCTGTATATTTGTTTATATATATATATATATATATATATATATATAT 1803
1641 AAGAGTTCAGATATGAGCTGTATATTTGTTTATATATATATATATATATATATATATATATAT 1700
1804 CATAACCATCAAAA 1817
1701 CATTACCCTCAAAA 1714

RESULT 17
IS-10-173-690-281
Sequence 281, Application US/10173690
Publication No. US20030166105A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C9
CURRENT APPLICATION NUMBER: US/10/173,690
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
IS-10-173-690-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
424 TTGGGCTGAGGCTCTGGGACTAAATGCGACTGGTGGTGGCCAGGCCCAAGACATGT 493
321 TGGGACTTCGGCTGCTCTGGTTCCTCCCTGGAATCCCGAGCTCGAGCCCGCCAGACATGT 380
484 TCTGCTCTTTTCCATCGGAAGAGATACTCCCGCGGAGAGCTGGCAACCTACTTTGGAGC 543
381 TCTGCTCTTTTCCATCGGAAGAGATACTCCCGCGGAGAGCTGGCAACCTACTTTGGAGC 440

544 CACAAGGCTGATGTACTTGCTGCTGTACTGCTGTACCTGTGTCAGAGGGCGGCCATGTGAGTTGTT 603
441 CACAAGGCTGATGTACTTGCTGCTGTACTGCTGTACCTGTGTCAGAGGGCGGCCATGTGAGTTGTT 500
604 ACCGCTTCCACTGTCCGCTGTCCACTGCGCCACGCTGTGA CGSAGGCCACAGCAATGCT 663
501 ACCGCTTCCACTGTCCGCTGTCCACTGCGCCACGCTGTGA CGSAGGCCACAGCAATGCT 560
664 GTCCCAAGTGTGTGGAACCTCACTCCCTCTGAGCTCCGCGGCCCAACCAAGTGTCTGCC 723
561 GTCCCAAGTGTGTGGAACCTCACTCCCTCTGAGCTCCGCGGCCCAACCAAGTGTCTGCC 620
724 AGCAAAACGGGACCAATGTACCAACAGSAGAGATCTTCAGTGGCCCATGAGCTGTCCCT 783
621 AGCAAAACGGGACCAATGTACCAACAGSAGAGATCTTCAGTGGCCCATGAGCTGTCCCT 680
784 CCGGCTTGCCCAACCAAGTGTGTCTCTGAGCTGCA CAGAGGGCCAGATCTACTCGGCC 843
681 CCGGCTTGCCCAACCAAGTGTGTCTCTGAGCTGCA CAGAGGGCCAGATCTACTCGGCC 740
844 TCACAACTGCCCCGACACAGGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 903
741 TCACAACTGCCCCGACACAGGCTGCCAGCACCCCTCCGCTGCCAGACTCTCTGCTGCC 800
904 AAGCTTGCAAGATGAGGCAAGTGAACAATCGATGAAGAGGACAGTGTGAGTGTGCTGCC 963
801 AAGCTTGCAAGATGAGGCAAGTGAACAATCGATGAAGAGGACAGTGTGAGTGTGCTGCC 860
964 ATGGGTGAGACATCTTCAGATTCATGTTCCAGTGTGCTGGGAGAAAAGAGGCGCGG 1023
861 ATGGGTGAGACATCTTCAGATTCATGTTCCAGTGTGCTGGGAGAAAAGAGGCGCGG 920
1024 GCACCCGAGCCGCCACTGGGCTCAGCGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
921 GCACCCGAGCCGCCACTGGGCTCAGCGGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
1084 CCAAGGGAGCGGAGGACACACTGTCAAGATCGCTCTGAGGAGAACATAGAAAGCT 1143
981 CCAAGGGAGCGGAGGACACACTGTCAAGATCGCTCTGAGGAGAACATAGAAAGCT 1040
1144 GTGTGATGGCGGAGAGAGCTACTCCACGGGAGGTGTGGCA CCGGCTTCCTGCTGCT 1203
1041 GTGTGATGGCGGAGAGAGCTACTCTCCA CGGGAGGTGTGGCA CCGGCTTCCTGCTGCT 1100
1204 TCGGCCCCCTTGCCCTGCACTCTATGCACCTGTGAGGATGGCCCGCAGGACTCCAGGTG 1263
1101 TCGGCCCCCTTGCCCTGCACTCTATGCACCTGTGAGGATGGCCCGCAGGACTCCAGGTG 1160
1264 TGACCTGTCCCAACGAGTACCCCTCGGCTCACCCCGAGAAAGTGGTGGGAAAGTGTGCA 1323
1161 TGACCTGTCCCAACGAGTACCCCTCGGCTCACCCCGAGAAAGTGGTGGGAAAGTGTGCA 1220
1324 AGATTTGCCCAGAGGACAAAGAGAGCCCTGGGCCACAGTGAATCACTTCTA CAGAGTGTG 1383
1221 AGATTTGCCCAGAGGACAAAGAGAGCCCTGGGCCACAGTGAATCACTTCTA CAGAGTGTG 1280
1384 CCAAGGACCCGGGCGGGTCTCTGTCACACATGGTATCCCAAGCCCAAGCAACCTGTC 1443
1281 CCAAGGACCCGGGCGGGTCTCTGTCACACATGGTATCCCAAGCCCAAGCAACCTGTC 1340
1444 GTGCTTTTCCCTGGAAACAGAGGCTCAGAGGCTGGAAGTACCTGGCCCAAGCCCAAGCAACCTGTC 1503
1341 GTGCTTTTCCCTGGAAACAGAGGCTCAGAGGCTGGAAGTACCTGGCCCAAGCCCAAGCAACCTGTC 1400
1504 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCCAAGCAACCTGTC 1563
1401 TAAAGATCAGGAACCTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGCCCAAGCAACCTGTC 1460
1564 AGAATCTTCCACTTGACCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1623
1461 AGAATCTTCCACTTGACCTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1520

RESULT 19
US-10-173-692-281
Sequence 281, Application US/10173692
Publication No. US20030166188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C20
CURRENT APPLICATION NUMBER: US/10/173,692
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
S-10-173-692-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Y 424 TTGGGCTGGAGCCTCTGGGACTAACTGGACATGCTGGTCTGGCCGCGGAGAGCTGGACATGT 483
b 321 TGGGACTGGGCTGCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 380
Y 484 TCTGCTTTTTCATGGGAGAGATATCTCCCGCGGAGAGCTGGACACCTTACTTTGGAGC 543
b 381 TCTGCTTTTTCATGGGAGAGATATCTCCCGCGGAGAGCTGGACACCTTACTTTGGAGC 440
Y 544 CACAAGGCTGATGATGCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 603
b 441 CACAAGGCTGATGATGCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGG 500
Y 604 ACCGCTCCACTGTCGGCTGTCCACTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 663
b 501 ACCGCTCCACTGTCGGCTGTCCACTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 560
Y 664 GTCCCAAGTGTGGAACTTCACTCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 723
b 561 GTCCCAAGTGTGGAACTTCACTCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 620
Y 724 AGCACAAGGAGACATGTACACACGGAGAGATCTTCACTGCTGGCTGCTGGCTGCTGGCTGCTGG 783
b 621 AGCACAAGGAGACATGTACACACGGAGAGATCTTCACTGCTGGCTGCTGGCTGCTGGCTGCTGG 680
Y 784 CCGGCTGCGCCAAACAAGTGTCTCTGAGCTGCAAGGAGAGATCTTCACTGCTGGCTGCTGGCTGCTGG 843
b 681 CCGGCTGCGCCAAACAAGTGTCTCTGAGCTGCAAGGAGAGATCTTCACTGCTGGCTGCTGGCTGCTGG 740
Y 844 TCACAACCTGCGCCGAAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
b 741 TCACAACCTGCGCCGAAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
Y 904 AAGCTTGAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
b 801 AAGCTTGAAGATGAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 860
Y 964 ATGGGTGAGATCTCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
b 861 ATGGGTGAGATCTCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 920

QY 1024 GCACCCAGCCGCCCACTGGGCTCAGCGGCCCTCTGAGGCTTCATCCCTGCGCACTTCAGAC 1083
Db 921 GCACCCAGCCGCCCACTGGGCTCAGCGGCCCTCTGAGGCTTCATCCCTGCGCACTTCAGAC 980
QY 1084 CCAAGGGAGCAGCAGCAGCAAACTGTCTCAAGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143
Db 981 CCAAGGGAGCAGCAGCAGCAAACTGTCTCAAGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1040
QY 1144 GTGTGATGCGGGGAGAGAGCTGCTCTCCACGCGGAGGTGTGGCCACCCGGGCTTCCCTGCTGCT 1203
Db 1041 GTGTGATGCGGGGAGAGAGCTGCTCTCCACGCGGAGGTGTGGCCACCCGGGCTTCCCTGCTGCT 1100
QY 1204 TCGGCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263
Db 1101 TCGGCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
QY 1264 TGACCTGTCTCCACCGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
Db 1161 TGACCTGTCTCCACCGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1220
QY 1324 AGATTTGCCCGAGAGAGCAAAAGCAGACCTCTGGCCACAGTGAAGTCACTTCTACAGGTGTC 1383
Db 1221 AGATTTGCCCGAGAGAGCAAAAGCAGACCTCTGGCCACAGTGAAGTCACTTCTACAGGTGTC 1280
QY 1384 CCAAGGCACCGGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1443
Db 1281 CCAAGGCACCGGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1340
QY 1444 GTGCTTTGCTG 1503
Db 1341 GTGCTTTGCTG 1400
QY 1504 TAAAGATGAGGAACTGAGGCTCAGAGAGTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1563
Db 1401 TAAAGATGAGGAACTGAGGCTCAGAGAGTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1460
QY 1564 AGATCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1623
Db 1461 AGATCTTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1520
QY 1624 CAGCACTTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1683
Db 1521 CAGCACTTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
QY 1684 ACCCTGAGCTGAAGGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1743
Db 1581 ACCCTGAGCTGAAGGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
QY 1744 AACAGTTCAGATATGAGCTGTATAATTTGTTTATTATATATATATATATATATATATATATATAT 1803
Db 1641 AACAGTTCAGATATGAGCTGTATAATTTGTTTATTATATATATATATATATATATATATATATAT 1700
QY 1804 CATTAACCATCAAAA 1817
Db 1701 CATTAACCTCAAAA 1714
RESULT 20
US-10-173-694-281
Sequence 281, Application US/10173694
Publication No. US20030166107A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C19
; CURRENT APPLICATION NUMBER: US/10/173,694
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-694-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGGCTGGAGCTCTCTGGGACTTAACATGTCAGTGTGGTGTTCAGAGCCCGACAGATGT 483
Db 321 TGGGACTCGGCTGTCTGTCTTCCCTCGACTCCACGCTCGAGCCCGGCGACAGATGT 380
Qy 484 TCTGCTTTTCCATGGAAGAGACTTCCCGCGGAGAGCTGGCACCTCTCTTGGAGC 543
Db 381 TCTGCTTTTCCATGGAAGAGACTTCCCGCGGAGAGCTGGCACCTCTCTTGGAGC 440
Qy 544 CACAAGGCTGATGTACTGCTGGCTGTACTGCTCAGAGGGGCGCCATGTAGTGT 603
Db 441 CACAAGGCTGTGTACTGCTGGCTGTACTGCTCAGAGGGGCGCCATGTAGTGT 500
Qy 604 ACCGCTTCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGGCCACAGCAATGT 663
Db 501 ACCGCTTCACTGTCCGCTGTCCACTGCCCCCAGCCTGTGACGAGGCCACAGCAATGT 560
Qy 664 GTCCCAAGTGTGGAACTCAGACTCTCTCTGAGTCTCCGCGCCCCCAGCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCAGACTCTCTCTGAGTCTCCGCGCCCCCAGCAAGTCTCTGCC 620
Qy 724 AGCAACGGGACCATGTACCAACACGAGGAGAGATCTCAGTGCCCATGAGCTGTCCCT 783
Db 621 AGCAACGGGACCATGTACCAACACGAGGAGAGATCTCAGTGCCCATGAGCTGTCCCT 680
Qy 784 CCGCTCTGCCCAACAGTGTCTCTGAGCTGTGCAAGAGGCCAGATCTACTGCGGCC 843
Db 681 CCGCTCTGCCCAACAGTGTCTCTGAGCTGTGCAAGAGGCCAGATCTACTGCGGCC 740
Qy 844 TCACAACCTGCCCCGAAACAGGCTGCCAGCAGCCCCCTCCCGTGCAGACTCTCTGTCTGCC 903
Db 741 TCACAACCTGCCCCGAAACAGGCTGCCAGCAGCCCCCTCCCGTGCAGACTCTCTGTCTGCC 800
Qy 904 AAGCTCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTCTCTCC 963
Db 801 AAGCTCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTCTCTCC 860
Qy 964 ATGGGTGAGACATCTCAGGATCCATGTTCCAGTGAATCTGGGAGAGAGAGGCCGG 1023
Db 861 ATGGGTGAGACATCTCAGGATCCATGTTCCAGTGAATCTGGGAGAGAGAGGCCGG 920
Qy 1024 GCACCCAGCCCCCAGCTGAGCTTCAATGTCAGTGTGAGTGTATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCAGCCCCCAGCTGAGCTTCAATGTCAGTGTGAGTGTATCCCTCGCCACTTCAGAC 980
Qy 1084 CCAAGGAGCAGGACAGCAACTGTCAAGATCTCTGAGGAGAGAAACATAAGAAAGCT 1143
Db 981 CCAAGGAGCAGGACAGCAACTGTCAAGATCTCTGAGGAGAGAAACATAAGAAAGCT 1040
Qy 1144 GTGTGATGGGGGAGAGAGCTACTCCAGGGGAGGTGTGGCACCCGCTTCCGTGCT 1203
Db 1041 GTGTGATGGGGGAGAGAGCTACTCCAGGGGAGGTGTGTGGCACCCGCTTCCGTGCT 1100
Qy 1204 TCGGCCCTTGTCCCTGATCTCTATGCACTGTGAGGATGGCCCGCAGACTGCGCAGGTG 1263
Db 1101 TCGGCCCTTGTCCCTGATCTCTATGCACTGTGAGGATGGCCCGCAGACTGCGCAGGTG 1160

RESULT 21
US-10-173-698-281
; Sequence 281, Application US/10173698
; Publication No. US20030166108A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C12
; CURRENT APPLICATION NUMBER: US/10/173,698
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-698-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;

Matches 1362; Conservative	0; Mismatches	32; Indels	0; Gaps	0;
424	TTGGGCTGGAGCCTCTGGAGCTAACTAGGACATCTGGTTCGGTTTGCCAGGCCGACAGATGTT	483		
321	TGGAGCTCGGCTGCTCTGGTCTCCCTTGGACTCCACGCTCGAGCCCGCCGACAGATGTT	380		
484	TCTGCCCTTTCCATGGGAAGAGATATCTCCCGCGAGAGCTGGGACCCCTACTTTGGAGC	543		
381	TCTGCCCTTTCCATGGGAAGAGATATCTCCCGCGAGAGCTGGGACCCCTACTTTGGAGC	440		
544	CACAAGGCTGTATGTACTGCTCTGCTGTACTCTCTCAGAGGGGCCCATGTGAGTTGTT	603		
441	CACAAGGCTGTATGTACTGCTCTGCTGTACTCTCTCAGAGGGGCCCATGTGAGTTGTT	500		
604	ACCGCTCTCACTGTCCGCTGTGCCATCTGCGCCCGAGCTGTGACGGAGCCACAGCAATGCT	663		
501	ACCGCTCTCACTGTCCGCTGTGCCATCTGCGCCCGAGCTGTGACGGAGCCACAGCAATGCT	560		
664	GTCCCAAGTGTGTGGAACTTCACTCTCTGAGCTCTCGGCGCCCACTAAAGTCTCTGCC	723		
561	GTCCCAAGTGTGTGGAACTTCACTCTCTGAGCTCTCGGCGCCCACTAAAGTCTCTGCC	620		
724	AGCACAAACGGGACCATGTATCCAAACGGAGAGATCTTCAGTGCCTCATGAGCTGTCTCCCT	783		
621	AGCACAAACGGGACCATGTATCCAAACGGAGAGATCTTCAGTGCCTCATGAGCTGTCTCCCT	680		
784	CCGCGCTGGCCGAAACGAGTGTCTCTGAGCTGCAAGAGGGCCAGATCTACTGGGCC	843		
681	CCGCGCTGGCCGAAACGAGTGTCTCTGAGCTGCAAGAGGGCCAGATCTACTGGGCC	740		
844	TCACAAGCTGCCCGGAAACGAGGTGCCGAGACCTCTCCCGTGCACAGATCTCTGTGTGCC	903		
741	TCACAAGCTGCCCGGAAACGAGGTGCCGAGACCTCTCCCGTGCACAGATCTCTGTGTGCC	800		
904	AAGCCTGTCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGCAAGTGTGCAATCGCTGCC	963		
801	AAGCCTGTCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGCAAGTGTGCAATCGCTGCC	860		
964	ATGGGCTGAGACATCTCTCAAGATCCATGTCTCAGTGTCTGGAGAAAGAGAGCCCGG	1023		
861	ATGGGCTGAGACATCTCTCAAGATCCATGTCTCAGTGTCTGGAGAAAGAGAGCCCGG	920		
1024	GCAATCCAGCCCTCACTGGCTCTCAGCGGCCCTCTGAGCTTCACTCCCTGGCACTTCAGAC	1083		
921	GCAATCCAGCCCTCACTGGCTCTCAGCGGCCCTCTGAGCTTCACTCCCTGGCACTTCAGAC	980		
1084	CAAAGGAGAGGAGCAGACAACTGTCAAGATGTCTCTGAAGGAGAAACATAAGAGAGCT	1143		
981	CAAAGGAGAGGAGCAGACAACTGTCAAGATGTCTCTGAAGGAGAAACATAAGAGAGCT	1040		
1144	GTGTGCAATGGCGGAGAGACCTACTCCACGGGAGGTGTGGCAACCGGCTTCCGTGCT	1203		
1041	GTGTGCAATGGCGGAGAGACCTACTCCACGGGAGGTGTGGCAACCGGCTTCCGTGCT	1100		
1204	TGGGCCCTTGGCTGATCTCTATGCACTGTGAGATGGCGCCAGAGATGCGCCAGCTG	1263		
1101	TGGGCCCTTGGCTGATCTCTATGCACTGTGAGATGGCGCCAGAGATGCGCCAGCTG	1160		
1264	TGACTGTCTCCACGAGTACCCTTCCGCTCACCCGAGAAAGTGTGCTGGGAGTGTCTGCA	1323		
1161	TGACTGTCTCCACGAGTACCCTTCCGCTCACCCGAGAAAGTGTGCTGGGAGTGTCTGCA	1220		
1324	AGATTTCGCCAGAGCAAAAGACAGACCTTGGCCACAGTACAGATCATGTTCTACACAGTGT	1383		
1221	AGATTTCGCCAGAGCAAAAGACAGACCTTGGCCACAGTACAGATCATGTTCTACACAGTGT	1280		
1384	CCAAAGGCAACGGGCGGGTCTCTGTCTCCACATCGGTATCCCCAAGCCGACCAACCTGCG	1443		
1281	CCAAAGGCAACGGGCGGGTCTCTGTCTCCACATCGGTATCCCCAAGCCGACCAACCTGCG	1340		
1444	GTGCTTTTGCCTTGGAAACAGAGGCTCTGGACTTGTGGAGATCTTACTCTCTGGAGCTGG	1503		
1341	GTGCTTTTGCCTTGGAAACAGAGGCTCTGGACTTGTGGAGATCTTACTCTCTGGAGCTGG	1400		

```

RESULT 22
US-10-173-699-281
/ Sequence 281, Application US/10173699
/ Publication No. US20030166109A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C8
/ CURRENT APPLICATION NUMBER: US/10/173,699
/ CURRENT FILING DATE: 2002-06-17
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 281
/ LENGTH: 1732
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-173-699-281

```

	Query Match	73.9%	Score 1342.8	DB 13	Length 1732	
	Best Local Similarity	97.7%	Prod. No. 0			
	Matches 1362	Conservative 0	Mismatches 32	Indels 0	Gaps 0	
QY	424	TTGGGCTGGAGCCTCTGGGACTAA	CA TGGCACTGTTCGTTTGCAGGCCAGACATGT	483		
DB	321	TGGACTCGCGCTGCTCTGTG	TCCCTTGGACTCCACGCTCGAGCCGGCCAGACATGT	380		
QY	484	CTCGCTTTTTCATGGGAAGAGAT	ACTCCCGCGGAGACTGGCACCCCTACTCTGGAGC	543		
DB	381	TTGCGCTTTTTCATGGGAAGAGAT	CTCCCGCGGAGACTGGCACCCCTACTCTGGAGC	440		
QY	544	CACAGGCTGTGATGTGCTGGCTGT	ACTCTGCTCAGAGGCGCCCACTGTGATGTT	603		
DB	441	CACAGGCTGTGATGTGCTGGCTGT	ACTCTGCTCAGAGGCGCCCACTGTGATGTT	500		
QY	604	ACCGCTCCACTGTTCGCGCTGTCT	CATGTCGCCCCCAAGCCTGTGACGAGGCCACACAAATGCT	663		

501 ACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCT 560
Qy 664 GTCCCAAGTGTGGAACTCACACTCCTCTGGACTCCGGGCCCCACCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCACACTCCTCTGGACTCCGGGCCCCACCAAGTCTCTGCC 620
Qy 724 AGCACAAGGACCACTGTACCAACAGGAGAGATCTTCAGTGCCCATGAGCTGTCCCT 783
Db 621 AGCACAAGGACCACTGTACCAACAGGAGAGATCTTCAGTGCCCATGAGCTGTCCCT 680
Qy 784 CCGGCTGCCCACCAAGTGTCTCTGAGCTGCAACAGGGGCCAGATCTACTGGGCC 843
Db 681 CCGGCTGCCCACCAAGTGTCTCTGAGCTGCAACAGGGGCCAGATCTACTGGGCC 740
Qy 844 TCACAACCTGCCCGAACAGGCTGCCAGACCCCTCCCGCTGCCAGATCTCTGTGCC 903
Db 741 TCACAACCTGCCCGAACAGGCTGCCAGACCCCTCCCACTGCCAGATCTCTGTGCC 800
Qy 904 AAGCTCTCAAGATGAGGCAAGTGTAGCAATCGGATCAAGAGACAGTGTGAGTCCCTCC 963
Db 801 AAGCTCTCAAGATGAGGCAAGTGTAGCAATCGGATCAAGAGACAGTGTGAGTCCCTCC 860
Qy 964 ATGGGTGAGACATCTCTAGATCCATGTTCCAGTGTCTGGGAGAAAGAGGGCCGG 1023
Db 861 ATGGGTGAGACATCTCTAGATCCATGTTCCAGTGTCTGGGAGAAAGAGGGCCGG 920
Qy 1024 GCACCCAGCCCACTGGCCCTCAGCCCTCAGCCCTCAGCTTCATCCCTGCGCACTTCAGAC 1083
Db 921 GCACCCAGCCCACTGGCCCTCAGCCCTCAGCTTCATCCCTGCGCACTTCAGAC 980
Qy 1084 CCAAGGAGGAGGAGCAGCAAACTGTCAAGATCTGTCTGAAGAGAAACATAAGAAAGCT 1143
Db 981 CCAAGGAGGAGGAGCAGCAAACTGTCAAGATCTGTCTGAAGAGAAACATAAGAAAGCT 1040
Qy 1144 GTGTGCAATGGGGAGAGAGTATCTCCACGGGAGGTGTGGCAACCGGCTTCCTGGTCT 1203
Db 1041 GTGTGCAATGGGGAGAGAGTATCTCCACGGGAGGTGTGGCAACCGGCTTCCTGGTCT 1100
Qy 1204 TGGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1263
Db 1101 TGGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 1160
Qy 1264 TGACCTGTCCCAACCGAGTACCCCTGCCCTCACCCTGAGAGAAAGTGGCTGGAGTGTGCA 1323
Db 1161 TGACCTGTCCCAACCGAGTACCCCTGCCCTCACCCTGAGAGAAAGTGGCTGGAGTGTGCA 1220
Qy 1324 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGTGAGATCTACAGAGTGTG 1383
Db 1221 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGTGAGATCTACAGAGTGTG 1280
Qy 1384 CCAAGGACCGGGCCGGCTCTGTCACACATCGGTATCCCAAGCCAGACCAACCTGC 1443
Db 1281 CCAAGGACCGGGCCGGCTCTGTCACACATCGGTATCCCAAGCCAGACCAACCTGC 1340
Qy 1444 GTGCTTTGCCCTGGAAACAGAGGCTGTG3ACTTTGGTGGAGATCTACCTCTGGAGCTGG 1503
Db 1341 GTGCTTTGCCCTGGAAACAGAGGCTGTG3ACTTTGGTGGAGATCTACCTCTGGAGCTGG 1400
Qy 1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCCCAAGGCCACACAGCC 1460
Qy 1564 AGAATCTTCCACTTGACTCAGATCAAGAACTCAGGAAAGCAAGATCTCCAGAAAGAGCA 1623
Db 1461 AGAATCTTCCACTTGACTCAGATCAAGAACTCAGGAAAGCAAGATCTCCAGAAAGAGCA 1520
Qy 1624 CAGCACTTCCGACTGTCTGCTGGCCGCCACGAGGTCAGTGGAAAGTCTCTTCTAGCCAG 1683
Db 1521 CAGCACTTCCGACTGTCTGCTGGCCGCCACGAGGTCAGTGGAAAGTCTCTTCTAGCCAG 1580
Qy 1684 ACCCTGAGCTGAAGGTCACGGCCAGTCCAGCAAAAGTGAACAGACATACAAAGACCT 1743
Db 1581 ACCCTGAGCTGAAGGTCACGGCCAGTCCAGCAAAAGTGAACAGACATACAAAGACCT 1640

RESULT 23

US-10-173-707-281

; Sequence 281, Application US/10173707

; Publication No. US20030186110A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zelin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P430R1C17

; CURRENT APPLICATION NUMBER: US/10/173,707

; PRIORITY FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 281

; LENGTH: 1732

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-173-707-281

Query Match

Best Local Similarity 73.9%; Score 1342.8; DB 13; Length 1732;

Matches 1382; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGCTGGAGCTTCTGGGACTAATGCGACTGTGCGCTTTGCGAGGCCACAGATGT 483
Db 321 TGGGACTCGCGCTGCTCTGCTTCCCTTGGACTCCACGCTCGAGCCGCCACAGATGT 380
Qy 484 TCTGCTTTTCCATGGGAAAGAGATATCTCCCGGCGAGAGCTGGCAACCTTCTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAAAGAGATATCTCCCGGCGAGAGCTGGCAACCTTCTGGAGC 440
Qy 544 CACAAGGCTGATGATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
Db 441 CACAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
Qy 604 ACGGCTTCACTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Db 501 ACGGCTTCACTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
Qy 664 GTCCCAAGTGTGGAACTCACAATCTCTCTGAGATCTCCGGGCCGCCCAAGTCTGCTGCC 723
Db 561 GTCCCAAGTGTGGAACTCACAATCTCTCTGAGATCTCCGGGCCGCCCAAGTCTGCTGCC 620
Qy 724 AGCACAACGGGACCACTGTACCAACACGGAGAGATCTTTCAGTGTCCCATGAGTGTTCCTCT 783
Db 621 AGCACAACGGGACCACTGTACCAACACGGAGAGATCTTTCAGTGTCCCATGAGTGTTCCTCT 680
Qy 784 CCGGCTGCCCAACCAAGTGTCTCTGAGTGTCTCTGAGTGTCTCTGAGTGTCTCTGAGTGTCTCT 843
Db 681 CCGGCTGCCCAACCAAGTGTCTCTGAGTGTCTCTGAGTGTCTCTGAGTGTCTCTGAGTGTCTCT 740
Qy 844 TCACAACCTGCCCGGAAACAGAGTGTCCAGCAACCTTCCGCTGCGACATCTCTGCTGCTGCC 903

741 TCACAACTGCCCCGAAACCAAGCTGGCCAGCAACCCCTCCCACTGCCAGACTCCTGCTGCC 800
904 AAGCTGCAAGAATGAGGCAAGTGAAGATCGATGAAAGAGGACAGTGTGCACTGCTGCC 963
801 AAGCTGCAAGAATGAGGCAAGTGAAGATCGATGAAAGAGGACAGTGTGCACTGCTGCC 860
964 ATGGGGTGAGACATCTCTCAGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG 1023
861 ATGGGGTGAGACATCTCTCAGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG 920
1024 GCACCCAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTCAGAC 1083
921 GCACCCAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTCAGAC 980
1084 CCAAGGAGAGGAGAGCAACATGTCAGATGCTCTGAAGAGAGAAACATAAGAACCTT 1143
981 CCAAGGAGAGGAGAGCAACATGTCAGATGCTCTGAAGAGAGAAACATAAGAACCTT 1040
1144 GTGTGATGCGCGGAGAGACGTAATCTCCACGCGGAGGTGTGGCAACCCGGCTTCCGTGCTT 1203
1041 GTGTGATGCGCGGAGAGACGTAATCTCCACGCGGAGGTGTGGCAACCCGGCTTCCGTGCTT 1100
1204 TCGGCCCCCTTGGCTTCATCTATGACCTGTGAGATGAGGATGAGGAGGAGGAGGAGGAG 1263
1101 TCGGCCCCCTTGGCTTCATCTATGACCTGTGAGATGAGGATGAGGAGGAGGAGGAGGAG 1160
1264 TGACCTGTCCACAGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGAAAGTGTGCA 1323
1161 TGACCTGTCCACAGAGTACCCCTGCGCTCACCCGAGAAAGTGGCTGGAAAGTGTGCA 1220
1324 AGATTGCCAGAGAGCAAAAGCAAGACCTGGCCACAGTGAATCAGTCTTACCAGGTGTC 1383
1221 AGATTGCCAGAGAGCAAAAGCAAGACCTGGCCACAGTGAATCAGTCTTACCAGGTGTC 1280
1384 CCAAGGAGAGGAGGAGGAGTCTGTCACATCGGTATCCCAAGCCAGCAACACCTGTC 1443
1281 CCAAGGAGAGGAGGAGGAGTCTGTCACATCGGTATCCCAAGCCAGCAACACCTGTC 1340
1444 GTGGCTTGGCTTGAACAGAGGAGGAGTGGAGTGGAGATCTACCTTGGAGAGCTGG 1503
1341 GTGGCTTGGCTTGAACAGAGGAGGAGTGGAGTGGAGATCTACCTTGGAGAGCTGG 1400
1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGGGCCCAAGGCCACACAGCC 1563
1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGTGAAGTACTGGGCCCAAGGCCACACAGCC 1460
1564 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1623
1461 AGAATCTTCCACTTGACTCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGGCA 1520
1624 CAGCACTTCCGACTGCTGCTGGCCGCCACGAGGTCATCTGGAGCTTCTTCCAGCCCG 1683
1521 CAGCACTTCCGACTGCTGCTGGCCGCCACGAGGTCATCTGGAGCTTCTTCCAGCCCG 1580
1684 ACCCTGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAGAAAGTGAAGGAGGAGGAGGAGGAG 1743
1581 ACCCTGAGCTGAAGGTCAAGGCTCAGGCTCAGCAAGAAAGTGAAGGAGGAGGAGGAGGAG 1640
1744 AACAGTTGAGATATGAGCTGATATTTGTTTATTAATATTAATTAATTAATTAAGAGTTG 1803
1641 AACAGTTGAGATATGAGCTGATATTTGTTTATTAATTAATTAATTAATTAAGAGTTG 1700
1804 CATAACCATCAAAA 1817
1701 CATTAACCCCTCAAAA 1714

RESULT 24
US-10-174-569-281
; Sequence 281, Application US/10174569
; Publication No. US2003016611A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian
APPLICANT: Deenoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William L.
APPLICANT: Zhang, Zemi
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: F430R1C39
CURRENT APPLICATION NUMBER: US/10/174,569
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-174-569-281
Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0; Mismatches 32; Indels 0; Gaps 0;
Matches 1362; Conservative 0;
QY 424 TTGGGCTGGAGGCTCTGGGACTAA CATGGCACTGGTCGGTTTGGCCAGGCCCAGACATGT 483
DB 321 TGGGACTCGCGCTGCTCTGGTTCCCTCCAGCTCCAGCGCTCGAGAGCCCGCCAGACATGT 380
QY 484 TCTGCTCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCAACCCCTACTTGGAGC 543
DB 381 TCTGCTCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCAACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGATGTACTGGCTGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTCTGT 603
DB 441 CACAAGGCTGATGTACTGGCTGGCTGTACTCTGCTCAGAGGGCGCCCATGTGAGTCTGT 500
QY 604 ACCTGCTTCACTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCT 663
DB 501 ACCTGCTTCACTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCT 560
QY 664 GTCCAAAGTGTGTGAACTCACTCCCTCTGAGTCCCGGGCCCAACCAAGTCTGCTGCC 723
DB 561 GTCCAAAGTGTGTGAACTCACTCCCTCTGAGTCCCGGGCCCAACCAAGTCTGCTGCC 620
QY 724 AGCAACAACGAGGACCATGTACCAACAGGAGAGATCTTCAGTGGCCCATGAGTGTTCCTCT 783
DB 621 AGCAACAACGAGGACCATGTACCAACAGGAGAGATCTTCAGTGGCCCATGAGTGTTCCTCT 680
QY 784 CCGCTGTCGCCCAACCAAGTGTCTCTGAGCTGTCAGAGTGCACAGAGGCGCAGATCTACTGCGCC 843
DB 681 CCGCTGTCGCCCAACCAAGTGTCTCTGAGCTGTCAGAGTGCACAGAGGCGCAGATCTACTGCGCC 740
QY 844 TCACAACTGCCCCGAAACCAAGCTGTCGCCAGCAACCCCTCCGCTGCCAGACTCTGCTGCC 903
DB 741 TCACAACTGCCCCGAAACCAAGCTGTCGCCAGCAACCCCTCCGCTGCCAGACTCTGCTGCC 800
QY 904 AAGCTGCAAGAATGAGGCAAGTGAAGATCGATGAAAGAGGACAGTGTGCACTGCTGCC 963
DB 801 AAGCTGCAAGAATGAGGCAAGTGAAGATCGATGAAAGAGGACAGTGTGCACTGCTGCC 860
QY 964 ATGGGGTGAGACATCTCTCAGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG 1023
DB 861 ATGGGGTGAGACATCTCTCAGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGG 920
QY 1024 GCACCCAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTCAGAC 1083
DB 921 GCACCCAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCACTTCAGAC 980
QY 1084 CCAAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1143

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C59
CURRENT APPLICATION NUMBER: US/10/175,736
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-736-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 424 TTGGGCTGGAGCTCTCGGAGTAACTGACATGTCAGTGTGTCAGGCGCCAGACATGT 483
DB 321 TGGGACTCGCGTCTCTGGTTCCTCGTACTCCACCTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCTTTTTCATGGGAAAGAGATCTCCCGCGGAGAGCTGGCAACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTTCATGGGAAAGAGATCTCCCGCGGAGAGCTGGCAACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGATGTACTGCTCGCTGTACTGCTCAGAGGGGCGCCCATGTGAGTTGTT 603
DB 441 CACAAGGCTGATGTACTGCTCGCTGTACTGCTCAGAGGGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTTCACTGTGCGCTGTCACCTGCCCCAGAGCTGTGAGGAGCCACAGCAATGCT 663
DB 501 ACCGCTTCACTGTGCGCTGTCACCTGCCCCAGAGCTGTGAGGAGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGGAACTTCACTCCCTTGGACTCCGGGCCCCCAAGTCTGCGC 723
DB 561 GTCCCAAGTGTGGAACTTCACTCCCTTGGACTCCGGGCCCCCAAGTCTGCGC 620
QY 724 AGCAACACGGGACCATGTACCAACACGGAGAGATCTTTCAGTCCCATAGCTTTCCCT 783
DB 621 AGCAACACGGGACCATGTACCAACACGGAGAGATCTTTCAGTCCCATAGCTTTCCCT 680
QY 784 CCGGCTTCCCAACACAGTGTGCTCTGCACTGTCACAGAGGGGCGCAGATCTACTGCGGCG 843
DB 681 CCGGCTTCCCAACACAGTGTGCTCTGCACTGTCACAGAGGGGCGCAGATCTACTGCGGCG 740
QY 844 TCACAACTGCGCCGACAGGCTGCCAGACCCCTCCGCTGCGCAGCTCTGCTGCGC 903
DB 741 TCACAACTGCGCCGACAGGCTGCCAGACCCCTCCCACTGCGCAGCTCTGCTGCGC 800
QY 904 AAGCTCGAAGATGAGGCAATGAGCAATCGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 963
DB 801 AAGCTCGAAGATGAGGCAATGAGCAATCGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
QY 964 ATGGGGTGAGACATCTCAGGATCCATGTTCCAGTGTGATCTGGGAGAGAGAGAGAGAGAG 1023
DB 861 ATGGGGTGAGACATCTCAGGATCCATGTTCCAGTGTGATCTGGGAGAGAGAGAGAGAGAG 920
QY 1024 GCACCCAGCCCCACATGGGCTCAGCGCCCTCTGAGCTTTCATCTCCCTCGCAGCTTCAGAC 1083
DB 921 GCACCCAGCCCCACATGGGCTCAGCGCCCTCTGAGCTTTCATCTCCCTCGCAGCTTCAGAC 980
QY 1084 CCAGGGAGAGGAGGAG 1143
DB 981 CCAGGGAGAGGAGGAG 1040
QY 1144 GTGTGATGGCGGAG 1203
DB 1041 GTGTGATGGCGGAG 1100
QY 1204 TCGGCCCCCTTGTGATCCCTATGCACTGTCAGTGTGAGGATGCGGCGCCAGGAGCTGCCAGCGTG 1263

DB 1101 TCGGCCCCCTTGTGATCCCTATGCACTGTGAGATGGCGCGGAGCTGCCAGCGTG 1160
QY 1264 TGACTCTGCCACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGCTGGAAAGTCTGCA 1323
DB 1161 TGACTCTGCCACCGAGTACCCCTGCGTCAACCCGAGAAAGTGGCTGGAAAGTCTGCA 1220
QY 1324 AGATTTGCCCAGAGAGACAAAGCAGACCTCGGCCACAGTGTGAGTCACTTCTACAGAGTGC 1383
DB 1221 AGATTTGCCCAGAGAGACAAAGCAGACCTCGGCCACAGTGTGAGTCACTTCTACAGAGTGC 1280
QY 1384 CCAAGGACCGGCGCGGCTCTGCTCCACATCGGTATCCCGAGCCCGAGCAACCTGC 1443
DB 1281 CCAAGGACCGGCGCGGCTCTGCTCCACATCGGTATCCCGAGCCCGAGCAACCTGC 1340
QY 1444 GTGCTTTGCCCTGGAAACACGAGGCTCGGACTTGGTGTGAGATCTACTCTGGAAGCTGG 1503
DB 1341 GTGCTTTGCCCTGGAAACACGAGGCTCGGACTTGGTGTGAGATCTACTCTGGAAGCTGG 1400
QY 1504 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAATACCTGGGCCCAAGGCCACACAGCC 1563
DB 1401 TAAAGATGAGGAAACTGAGGCTCAGAGAGGTGAATACCTGGGCCCAAGGCCACACAGCC 1460
QY 1564 AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1623
DB 1461 AGAATCTTCCACTTGAATCAGATCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAGAAAGTCA 1520
QY 1624 GAGCATCTCGACTGCTGCTGGGCCCCGACGAAAGTCACTGGAAGCTTCTTCTAGCCAG 1683
DB 1521 GAGCATCTCGACTGCTGCTGGGCCCCGACGAAAGTCACTGGAAGCTTCTTCTAGCCAG 1580
QY 1684 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT 1743
DB 1581 ACCCTGGAGCTGAAGGTCAAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCT 1640
QY 1744 AACCTTGCAGATATCAGCTGTATTAATTTGTTTATATATATATATATATATATATATATAT 1803
DB 1641 AACCTTGCAGATATCAGCTGTATTAATTTGTTTATATATATATATATATATATATATATAT 1700
QY 1804 CATACACCTCAAAA 1817
DB 1701 CATACACCTCAAAA 1714

RESULT 30

US-10-175-742-281
Sequence 281, Application US/10175742
Publication No. US2003016118A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C59
CURRENT APPLICATION NUMBER: US/10/175,742
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-742-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732; Best Local Similarity 97.7%; Pred. No. 0; Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;									
QY	424	TTGGGCTTGGAGGCTCTCTGGGACTAAACATGGCACTGTGTGGTTTCCAGGCGCCAGACATGT	483						
DB	321	TGGGACTCGCGTGTCTGTGGTTCCCTCGGACTCCACGCTCGAGCCGCGCCAGACATGT	380						
QY	484	TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	543						
DB	381	TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGGAGAGCTGGCACCCCTACTTTGGAGC	440						
QY	544	CACAGGCGCTGATGTACTGCTGGCTGTACTGTCTCAGAGGGCGCCCATGTGAGTTGTT	603						
DB	441	CACAGGCGCTGATGTACTGCTGGCTGTACTGTCTCAGAGGGCGCCCATGTGAGTTGTT	500						
QY	604	ACGCGCTTCACTGTCCGCTGTCTCACTGGCCCCAGCCTGTGACGAGGCCACAGCAATGCT	663						
DB	501	ACGCGCTTCACTGTCCGCTGTCTCACTGGCCCCAGCCTGTGACGAGGCCACAGCAATGCT	560						
QY	664	GTCCCAAGTGTGGAACTCTCAGACTCCCTCTGGACTCCGCGGCCCCACCAAGTCTCTGCC	723						
DB	561	GTCCCAAGTGTGGAACTCTCAGACTCCCTCTGGACTCCGCGGCCCCACCAAGTCTCTGCC	620						
QY	724	AGCACACGGGACCATGTACCAACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT	783						
DB	621	AGCACACGGGACCATGTACCAACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCTCT	680						
QY	784	CCGCGCTGCCCAACCAAGTGTGTCTCTGAGCTGACAGAGGCCAGATCTACTCGGGCC	843						
DB	681	CCGCGCTGCCCAACCAAGTGTGTCTCTGAGCTGACAGAGGCCAGATCTACTCGGGCC	740						
QY	844	TCACAACTCTCCCGCCGAAACAGGCTGCCAGCACCTCTCCGCTCCGACAGATCTCTCTGCC	903						
DB	741	TCACAACTCTCCCGCCGAAACAGGCTGCCAGCACCTCTCCGCTCCGACAGATCTCTCTGCC	800						
QY	904	AAGCTCTCAAAGATAGGACCAAGTACAGCAATCGAGTGAAGAGACAGTGTGAGTCTGCCCT	963						
DB	801	AAGCTCTCAAAGATAGGACCAAGTACAGCAATCGAGTGAAGAGACAGTGTGAGTCTGCCCT	860						
QY	964	ATGGGCTGAGACATCTCAGATCTATGTTTCCAGTGTGCTGGGAGAGAGAGGCGCG	1023						
DB	861	ATGGGCTGAGACATCTCAGATCTATGTTTCCAGTGTGCTGGGAGAGAGAGGCGCGG	920						
QY	1024	GCACCCAGCCCCCACTGGCTTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTTCAGAC	1083						
DB	921	GCACCCAGCCCCCACTGGCTTCAGCGCCCTCTGAGCTTCACTCCCTCGCCACTTCAGAC	980						
QY	1084	CAAAGGAGCAGGACGACCAACTGTCAAGATCTCTGAAGAGAAACATAAGAAAGCT	1143						
DB	981	CAAAGGAGCAGGACGACCAACTGTCAAGATCTCTGAAGAGAAACATAAGAAAGCT	1040						
QY	1144	GTGTGATGCGGGAAGAGTACTCCACGGGAGGTGTGGACCCGCGCTTCGCTGCT	1203						
DB	1041	GTGTGATGCGGGAAGAGTACTCCACGGGAGGTGTGGACCCGCGCTTCGCTGCT	1100						
QY	1204	TGCGCCCTTGCCTGCACTCTATGCACTGTGAGGATGGCGCCAGGATGCAAGCGTG	1263						
DB	1101	TGCGCCCTTGCCTGCACTCTATGCACTGTGAGGATGGCGCCAGGATGCAAGCGTG	1160						
QY	1264	TGACTGTCTCCACCGAGTACCCCTGCCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA	1323						
DB	1161	TGACTGTCTCCACCGAGTACCCCTGCCGTCAACCCCGAGAAAGTGGCTGGGAAGTGTGCA	1220						
QY	1324	AGATTTCCCGCAGAGCAAGACGACCCCTGGCCACAGTGAATCACTTACCAAGTGTG	1383						
DB	1221	AGATTTCCCGCAGAGCAAGACGACCCCTGGCCACAGTGAATCACTTACCAAGTGTG	1280						
QY	1384	CCAAAGGACCGGGCGGGTCTGTGTCACACATCTGGTATCCCGAAGGCCACAGCACTTGC	1443						
DB	1281	CCAAAGGACCGGGCGGGTCTGTGTCACACATCTGGTATCCCGAAGGCCACAGCACTTGC	1340						
QY	1444	GTGCGTTTGGCCCTGGAAACAGAGGCGCTCGGACTTGTGTGGAGATCTACTCTTGGAACTGG	1503						

RESULT 31

US-10-175-744-281
; Sequence 281, Application US/10175744
; Publication No. US20030166119A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C49
; CURRENT APPLICATION NUMBER: US/10/175,744
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-744-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 424 TTGGGCTTGGAGGCTCTCTGGGACTAAACATGGCACTGTGTGGTTTCCAGGCGCCAGACATGT 483
DB 321 TGGGACTCGCGTGTCTGTGGTTCCCTCGGACTCCACGCTCGAGCCGCGCCAGACATGT 380
QY 484 TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGGAGAGTGGCACCCCTACTTTGGAGC 543
DB 381 TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGGAGAGTGGCACCCCTACTTTGGAGC 440
QY 544 CACAGGCGCTGATGTACTGCTGGCTGTACTGTCTCAGAGGGCGCCCATGTGAGTTGTT 603
DB 441 CACAGGCGCTGATGTACTGCTGGCTGTACTGTCTCAGAGGGCGCCCATGTGAGTTGTT 500

604 ACCGCTCCACTGTCGCGCTGTCCACTGCCCCAGCGCTGTGACGAGGCCACAGCAATGCT 663
Db ACCGCTCCACTGTCGCGCTGTCCACTGCCCCAGCGCTGTGACGAGGCCACAGCAATGCT 560
664 GTCCCAAGTGTGTGAACCTCACACTCCCTCGAGCTCCGGGCCCCCAACAAAGTCTCTGCC 723
Db GTCCCAAGTGTGTGAACCTCACACTCCCTCGAGCTCCGGGCCCCCAACAAAGTCTCTGCC 620
724 AGCACAAGGACCATGTACACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCCT 783
Db AGCACAAGGACCATGTACACACGAGAGATCTTCAGTGCCCATGAGCTGTTCCCT 580
784 CCGCGCTGCCAAACCAAGTGTCTGTGAGCTGCAACAGAGGCCCAATCTACTGCGGCC 843
Db CCGCGCTGCCAAACCAAGTGTCTGTGAGCTGCAACAGAGGCCCAATCTACTGCGGCC 740
844 TCACAACTGCGCCCGAACACAGCGCTGCCAGCAGCCCTCCCGCTGCGAGACTCTCTGCTGCC 903
Db TCACAACTGCGCCCGAACACAGCGCTGCCAGCAGCCCTCCCGCTGCGAGACTCTCTGCTGCC 800
904 AAGCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTCCCTCC 963
Db AAGCTGCAAGATGAGGCAAGTGAAGCAATCGATGAAGAGACAGTGTGAGTCCCTCC 860
964 ATGGGGTGAACATCTCTAGATCATGTTCAGTGTGCTGGAGAGAGAGGCCGCG 1023
Db ATGGGGTGAACATCTCTAGATCATGTTCAGTGTGCTGGAGAGAGAGAGGCCGCG 920
1024 GCACCCAGCCCCACTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCACTTCAGAC 1083
Db GCACCCAGCCCCACTGCGCTCAGCGCCCTCTGAGCTTCATCCCTGCGCACTTCAGAC 980
1084 CCAAGGAGCAGGACAGCACTGTCAAGATGCTCTGAGGAGAGAAACATAAGAAAGCT 1143
Db CCAAGGAGCAGGACAGCACTGTCAAGATGCTCTGAGGAGAGAAACATAAGAAAGCT 1040
1144 GTGTGCAATGGCGGAGAGTACTCCACGGGAGGTGTGGCACCGGCTTCGCTGCT 1203
Db GTGTGCAATGGCGGAGAGTACTCCACGGGAGGTGTGGCACCGGCTTCGCTGCT 1100
1204 TCGGCCCCCTTGCCTGATCTATGCACTGTGAGGATGGCGCGCAGAGCTTGCACAGGTG 1263
Db TCGGCCCCCTTGCCTGATCTATGCACTGTGAGGATGGCGCGCAGAGCTTGCACAGGTG 1160
1264 TGACTGTCCACCGAGTACCCCTCCCTGCTCACCAGGAAAGTGGCTGGAGGTGCTGCA 1323
Db TGACTGTCCACCGAGTACCCCTCCCTGCTCACCAGGAAAGTGGCTGGAGGTGCTGCA 1220
1324 AGATTGCGCAGAGGACAAAGCAGACCTGCGCACAGTGAATCAGTTCTACAGGTGTG 1383
Db AGATTGCGCAGAGGACAAAGCAGACCTGCGCACAGTGAATCAGTTCTACAGGTGTG 1280
1384 CMAAGGACACGGGCGCGGTCTGTGTCACATCGGTATCCCGAGCCGACAGCACTGCG 1443
Db CMAAGGACACGGGCGCGGTCTGTGTCACATCGGTATCCCGAGCCGACAGCACTGCG 1340
1444 GTGCTTTGCCCTTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1503
Db GTGCTTTGCCCTTGGAAACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAGCTGG 1400
1504 TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCGCCCAAGGCCACACAGCC 1563
Db TAAAGATGAGAAACTGAGGCTCAGAGAGTGAAGTACCTGGCGCCCAAGGCCACACAGCC 1460
1564 AGATCTCCACTTGAATCAGATCAAGAAAGTCAGGAGCAAGACTTCCAGAAAGAGGCA 1623
Db AGATCTCCACTTGAATCAGATCAAGAAAGTCAGGAGCAAGACTTCCAGAAAGAGGCA 1520
1624 CAGCACTTCGAGTGTGCTGCGTGGCGCCCAAGAGGTCACTGGAACTTCTCTAGCCAG 1683
Db CAGCACTTCGAGTGTGCTGCGTGGCGCCCAAGAGGTCACTGGAACTTCTCTAGCCAG 1580
1684 ACCCTGAGCTGAGGCTCAGGCGCTCAGTCCAGACAAAGTGACCAAGACATACAAAGACCT 1743

Db 1581 ACCCTGAGCTGAAGTCCAGGCCAGTCCAGCAAGTGTACCAAGCATACCAAGCT 1640
Qy 1744 AACAGTTGCCAGATGAGCTGTATAATTTGTTATTAATATAAATAAGATTG 1803
Db 1641 AACAGTTGCCAGATGAGCTGTATAATTTGTTATTAATATAAATAAGATTG 1700
Qy 1804 CATACCATCAAAA 1817
Db 1701 CATACCATCAAAA 1714

RESULT 32
US-10-175-745-281
; Sequence 281, Application US/10175745
; Publication No. US20030166120A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C55
; CURRENT APPLICATION NUMBER: US/10/175,745
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-745-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 424 TTGGGCTGGAGCTCTCTGGGACTTAACATGGCACTGGTCGCTTTCGAGGCCACAGATGT 483
Db 321 TGGGACTCGCGCTCTCTCTGTTCCCTTCGACTCCACGCTCGAGCCGCCACAGATGT 380
Qy 484 TCTGCTTTTCCATGGGAAGAGATATCTCCCGCGAGAGCTGGCACCTTACTTTGGAGC 543
Db 381 TCTGCTTTTCCATGGGAAGAGATATCTCCCGCGAGAGCTGGCACCTTACTTTGGAGC 440
Qy 544 CACAGGCTCATGCTACTGCTGCGCTGTACTGCTCAGAGGCGGCCCATGTGAGTTGTT 603
Db 441 CACAGGCTCATGCTACTGCTGCGCTGTACTGCTCAGAGGCGGCCCATGTGAGTTGTT 500
Qy 604 ACCGCTCAGCTTCGCGCTGCTCCATCGCCCGAGAGCTGTCGAGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCAGCTTCGCGCTGCTCCATCGCCCGAGAGCTGTCGAGGAGCCACAGCAATGCT 560
Qy 664 GTCCCAAGTGTGTGGAACCTTCACTCCCTCTGAGCTCCGGGCCCCCAAGTCTCTGCC 723
Db 561 GTCCCAAGTGTGTGGAACCTTCACTCCCTCTGAGCTCCGGGCCCCCAAGTCTCTGCC 620
Qy 724 AGCACAAGGAGACCATGTACAAACGAGAGATCTTTCAGTGCCCATGAGCTGTTCCCT 783
Db 621 AGCACAAGGAGACCATGTACAAACGAGAGATCTTTCAGTGCCCATGAGCTGTTCCCT 680
Qy 784 CCGCTCTGCCAAACAGTGTGCTCTGAGCTGCAACAGGAGGCCAGATCTTACTGCGGCC 843
Db 681 CCGCTCTGCCAAACAGTGTGCTCTGAGCTGCAACAGGAGGCCAGATCTTACTGCGGCC 740

1324 AGATTGGCCGAGGAGCAAGCAGACCTCGGCCACAGTGAGATCAGTTCTACAGGTGTC 1383
1221 AGATTGGCCGAGGAGCAAGCAGACCTCGGCCACAGTGAGATCAGTTCTACAGGTGTC 1280
1384 CCAAGGCAACCGGCGCGGTCTCGTCCACACATCGGTAATCCCAAGCCCAAGACCTGTC 1443
1281 CCAAGGCAACCGGCGCGGTCTCGTCCACACATCGGTAATCCCAAGCCCAAGACCTGTC 1340
1444 GTGCGCTTTCGCTCGGAAACAGAGGCTCGGACTTGGTGAGATCTACCTCTCGAAGCTGG 1503
1341 GTGCGCTTTCGCTCGGAAACAGAGGCTCGGACTTGGTGAGATCTACCTCTCGAAGCTGG 1400
1504 TAAAGATGAGAAACTGAGCTCAGAGAGGTGAAGTACCTGGGCCCAAGGCCACACAGCC 1563
1401 TAAAGATGAGAAACTGAGCTCAGAGAGGTGAAGTACCTGGGCCCAAGGCCACACAGCC 1460
1564 AGAATCTTCCATTGACCTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGSCA 1623
1461 AGAATCTTCCATTGACCTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGGSCA 1520
1624 CAGCACTTCCGAGCTCTCGTGGGCCCCCAAGAGTCACTGGAACGTCTTCTAGCCCCAG 1683
1521 CAGCACTTCCGAGCTCTCGTGGGCCCCCAAGAGTCACTGGAACGTCTTCTAGCCCCAG 1580
1684 ACCTGGAGCTCAAGGTCAGGGCCAGTCCAGACAAAGTGACCCAGACATAACAAAGACCT 1743
1581 ACCTGGAGCTCAAGGTCAGGGCCAGTCCAGACAAAGTGACCCAGACATAACAAAGACCT 1640
1744 AACAGTTGAGATATGAGCTGTATTAATTTGTTTATATATATTAATTAAGAAAGTTG 1803
1641 AACAGTTGAGATATGAGCTGTATTAATTTGTTTATATATATTAATTAAGAAAGTTG 1700
1804 CATAACCTCAAAA 1817
1701 CATTACCTCAAAA 1714

RESULT 35
IS-10-175-754-281
Sequence 281, Application US/10175754
Publication No. US20030166123A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C58
CURRENT APPLICATION NUMBER: US/10/175,754
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 281
LENGTH: 1732
TYPE: DNA
ORGANISM: Homo Sapien
IS-10-175-754-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
424 TTGGGCTGAGAGCTCTGGAGCTAAATGGCATCTGGTGGTTGGCAGGCCCAACAGATGT 483
321 TGGGATCTCGCGTGTCTGGTTCCCTCGACTCCACAGCTCGAGCCGCCCAAGCATGT 360

QY 484 TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGCAGAGCTGGCACCCCTACTTGGAGC 543
DB 381 TCTGCTTTTTCATGGGAAGAGATACCTCCCGGGCAGAGCTGGCACCCCTACTTGGAGC 440
QY 544 CACAAGGCTGTATGTACTGCTCGGTGTACTCTGCTCAGAGGGCGCCCATGTGATGTTGT 603
DB 441 CACAAGGCTGTATGTACTGCTCGGTGTACTCTGCTCAGAGGGCGCCCATGTGATGTTGT 500
QY 604 ACCGCTTCCACTGTCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
DB 501 ACCGCTTCCACTGTCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 560
QY 664 GTCCAAAGTTGTGGAACTCTCACTCCCTCTGGAATCTCCGGGCCCAACAAAGTCTGCTGCC 723
DB 561 GTCCAAAGTTGTGGAACTCTCACTCCCTCTGGAATCTCCGGGCCCAACAAAGTCTGCTGCC 620
QY 724 AGCAACAACGGGACCTATGTATCAACACAGAGAGATCTTTCAGTGGCCCATGAGCTGTGCCCT 783
DB 621 AGCAACAACGGGACCTATGTATCAACACAGAGAGATCTTTCAGTGGCCCATGAGCTGTGCCCT 680
QY 784 CCGGCTTGGCCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 843
DB 681 CCGGCTTGGCCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
QY 844 TCACAACCTTGGCCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 903
DB 741 TCACAACCTTGGCCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
QY 904 AAGCTTGCAAAAGATGAGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCTGCTGCTGCTGCT 963
DB 801 AAGCTTGCAAAAGATGAGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCTGCTGCTGCTGCT 860
QY 964 ATGGGTTGAGACATCTCTCAGGATCCCATGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGT 1023
DB 861 ATGGGTTGAGACATCTCTCAGGATCCCATGTTCAGTGTTCAGTGTTCAGTGTTCAGTGTTCAGTGT 920
QY 1024 GCACCCGAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
DB 921 GCACCCGAGCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
QY 1084 CCAAGGGAACAGGCAAGCACTGTCAGATCTCTGAGAGGAAGAACTAAGAAAGCT 1143
DB 981 CCAAGGGAACAGGCAAGCACTGTCAGATCTCTGAGAGGAAGAACTAAGAAAGCT 1040
QY 1144 GTGTGATGGCGGGAAGACGTAATCCACGCGGAGGTGTGGCAACCCGGCTTCCGTGCT 1203
DB 1041 GTGTGATGGCGGGAAGACGTAATCCACGCGGAGGTGTGGCAACCCGGCTTCCGTGCT 1100
QY 1204 TCGGCCCCCTTGGCTGATCTATGCACTGTGAGGATGGCGCCGAGGACTCCAGCGTG 1263
DB 1101 TCGGCCCCCTTGGCTGATCTATGCACTGTGAGGATGGCGCCGAGGACTCCAGCGTG 1160
QY 1264 TGACCTGTCCCAAGGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
DB 1161 TGACCTGTCCCAAGGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1220
QY 1324 AGATTTGCCAGAGGACAAAGCAGACCTTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1383
DB 1221 AGATTTGCCAGAGGACAAAGCAGACCTTGGCCACAGTGAGATCAGTTCTACAGGTGTC 1280
QY 1384 CCAAGGCAACCGGCGCGGTCTCTGCTCCACACATCGGTATCCCAAGCCCAAGCAACCTGTC 1443
DB 1281 CCAAGGCAACCGGCGCGGTCTCTGCTCCACACATCGGTATCCCAAGCCCAAGCAACCTGTC 1340
QY 1444 GTGCTTTCGCTTGGAAACAGAGGCTCTGGAGATCTACCTCTCGAAGCTGG 1503
DB 1341 GTGCTTTCGCTTGGAAACAGAGGCTCTGGAGATCTACCTCTCGAAGCTGG 1400
QY 1504 TAAAGATGAGAAACTGAGGCTCAGAGGTTGAAGTACCTGGGCCCAAGGCCCAACAGCC 1563
DB 1401 TAAAGATGAGAAACTGAGGCTCAGAGGTTGAAGTACCTGGGCCCAAGGCCCAACAGCC 1460

; APPLICANT: Pan,James		1204	TCGGCCCTTGCCCTGCATCTCTATGCACTGTGAGGATGGCCGACAGACTTGCCAGCGTG	1263
; APPLICANT: Smith,Victoria		QY		
; APPLICANT: Watanabe,Colin K.		Db		
; APPLICANT: Wood,William I.		1101	TCGGCCCTTGCCCTGCATCTCTATGCACTGTGAGGATGGCCGACAGACTTGCCAGCGTG	1160
; APPLICANT: Zhang,Zemin		QY		
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC		1264	TGACCTGTGCCACACAGTAGTACCTCTGCGGTCACTCCGAGAAAGTGGCTGGGAAGTGTGCA	1323
; FILE REFERENCE: P3430R1C85		Db		
; CURRENT APPLICATION NUMBER: US/10/176,754		1161	TGACCTGTGCCACACAGTAGTACCTCTGCGGTCACTCCGAGAAAGTGGCTGGGAAGTGTGCA	1220
; CURRENT FILING DATE: 2002-06-20		QY		
; Prior Application removed - See File Wrapper or Palm		1324	AGATTTCGCCCAGAGGACABAGCAGACCTGSCCACAAGTGCAGATCAGTTTCTACAGAGTGTG	1383
; NUMBER OF SEQ ID NOS: 612		Db		
; SEQ ID NO 281		1221	AGATTTCGCCCAGAGGACABAGCAGACCTGSCCACAAGTGCAGATCAGTTTCTACAGAGTGTG	1280
; LENGTH: 1732		QY		
; TYPE: DNA		1384	CCAGGACACGGGCGGGTTCCTGTCACACATCGGTATCCCAAGGCCAGACACCTGC	1443
; ORGANISM: Homo Sapien		Db		
US-10-176-754-281		1281	CCAGGACACGGGCGGGTTCCTGTCACACATCGGTATCCCAAGGCCAGACACCTGC	1340
Query Match		QY		
Best Local Similarity 97.7%; Pred. No. 0;		1444	GTGCTTTTGGCCCTGGAACACAGAGGCTCGGACTTGGAGATCTACCTCTGGAAGCTGG	1503
Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;		Db		
424 TTGGGCTGGAGCTCCTTGGAATACATGCACTGCTCGGTTTGGCCAGGCCAGACATGT		QY		483
321 TGGGACTCGGCTGCTCTGGTCCCTGAGTCCCACTCGCTCGAGCCGCGCCAGACATGT		Db		380
484 TTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACTTCTGGAGC		QY		543
381 TCTGCTTTTCCATGGGAAGAGATACTCCCGCGGAGAGCTGGCACTTCTGGAGC		Db		440
544 CACAAGGCTGATGTACTCGCTGCTGTACTGCTCAGAGGGGCGCCCATGTGAGTTGT		QY		603
441 CACAAGGCTGATGTACTCGCTGCTGTACTGCTCAGAGGGGCGCCCATGTGAGTTGT		Db		500
604 ACCGCTCCACTGTCGGCTGTCTCACTGCCCCAGAGCTGTGACGAGGCCACAGCAATGT		QY		663
501 ACCGCTCCACTGTCGGCTGTCTCACTGCCCCAGAGCTGTGACGAGGCCACAGCAATGT		Db		560
664 GTCCCAAGTGTGGAACTCACTCCCTCTGATCTCGGCGGCCACCAAGTCTCTGCC		QY		723
561 GTCCCAAGTGTGGAACTCACTCCCTCTGATCTCGGCGGCCACCAAGTCTCTGCC		Db		620
724 AGCAACAGGGAACAATGTACCAACAGGAGAGATCTTACGTGCCCATGAGTGTCCCT		QY		783
621 AGCAACAGGGAACAATGTACCAACAGGAGAGATCTTACGTGCCCATGAGTGTCCCT		Db		680
784 CCGGCTGCCCAACCAAGTGTCTCTGAGCTGCAAGAGGGCCAGATCTACTGCGGCC		QY		843
681 CCGGCTGCCCAACCAAGTGTCTCTGAGCTGCAAGAGGGCCAGATCTACTGCGGCC		Db		740
844 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCGCTGCCAGACTCTCTGTGCC		QY		903
741 TCACAACCTGCCCCGAAACAGGCTGCCAGACCCCTCCGCTGCCAGACTCTCTGTGCC		Db		800
904 AAGCTCGAAGATGAGGCAAGTGAAGCAATCGATGAGAGACAGTGTGAGTCTGCTCC		QY		963
801 AAGCTCGAAGATGAGGCAAGTGAAGCAATCGATGAGAGACAGTGTGAGTCTGCTCC		Db		860
964 ATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTATGCTGGGAGAAAGAGAGGCCGG		QY		1023
861 ATGGGGTGAGACATCTCTCAGGATCCATGTTCCAGTGTATGCTGGGAGAAAGAGAGGCCGG		Db		920
1024 GACCCAGCCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC		QY		1083
921 GACCCAGCCCCACTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC		Db		980
1084 CCAGGGAGCAGGACGACATCTGATCAGATCTCTGAGAGGAAACATGAGAAAGCTT		QY		1143
981 CCAGGGAGCAGGACGACATCTGATCAGATCTCTGAGAGGAAACATGAGAAAGCTT		Db		1040
1144 GTGTGATGGCGGGAACAATGATCCCAAGGGAGGTGTGGACCCCGGCTTCGCTGCT		QY		1203
1041 GTGTGATGGCGGGAACAATGATCCCAAGGGAGGTGTGGACCCCGGCTTCGCTGCT		Db		1100

RESULT 39
US-10-176-755-281
; Sequence 281, Application US/10176755
; Publication No. US20030166127A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C106
; CURRENT APPLICATION NUMBER: US/10/176,755
; PRIOR FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-176-755-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732; Best Local Similarity 97.7%; Pred. No. 0; Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;			
QY	424	TTGGGCTTGAGGCTCTCTGGGACTAAATGAGCACTGGTTCGGTTTCAGGCGCCAGACATGT	483
Db	321	TGGGACTCTGGGCTGTCTGTGTCTCCCTTGAGCTCCACGCTCGAGCCCGCCAGACATGT	380
QY	484	TCTGCTTTTTCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC	543
Db	381	TCTGCTTTTTCATGGGAGAGATATCTCCCGCGGAGAGCTGGCACCCCTACTTGGAGC	440
QY	544	CACAGGCGCTGATGTACTGCTGCTGGCTGTACTCTCTCAGAGGCGCCCAATGTGAGTTGT	603
Db	441	CACAGGCGCTGATGTACTGCTGCTGGCTGTACTCTCTCTCAGAGGCGCCCAATGTGAGTTGT	500
QY	604	ACCGCTTCCACTGTCCGCTGTCCACTGTCCGCTGTCCGCTGTCCGCTGTCCGCTGTCCGCT	663
Db	501	ACCGCTTCCACTGTCCGCTGTCCACTGTCCGCTGTCCGCTGTCCGCTGTCCGCTGTCCGCT	560
QY	664	GTCCCAAGTGTGGAACTCCTCAGCTCCCTCTGGACTCCGCGGCCACCAAGTCTCTGCC	723
Db	561	GTCCCAAGTGTGTGAACTCTCACTCTCTCTGAGCTTCGCGGCCACCAAGTCTCTGCC	620
QY	724	AGCAACAGGACCATGTATCCAAACAGGAGAGATCTTCACTGCTCCATGAGCTGTTCCTCT	783
Db	621	AGCAACAGGACCATGTATCCAAACAGGAGAGATCTTCACTGCTCCATGAGCTGTTCCTCT	680
QY	784	CCGCTGTGCCAACAGATGTGTCTCTCTGAGCTGTGACAGAGGCGCCAGATCTACTCGGCC	843
Db	681	CCGCTGTGCCAACAGATGTGTCTCTCTGAGCTGTGACAGAGGCGCCAGATCTACTCGGCC	740
QY	844	TCACAACTGCCGCCAAACAGGCTGCCAGACCCCTCCGCTGCCAGACTCTCTCTGCC	903
Db	741	TCACAACTGCCGCCAAACAGGCTGCCAGACCCCTCCGCTGCCAGACTCTCTCTGCC	800
QY	904	AAGCTGTCAAGATGAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	963
Db	801	AAGCTGTCAAGATGAGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	860
QY	964	ATGGGTGTAGATCTCTCAGATCTCTCAGTGTGATGTCTGGAGAAAGAGAGGCCGG	1023
Db	861	ATGGGTGTAGATCTCTCAGATCTCTCAGTGTGATGTCTGGAGAAAGAGAGGCCGG	920
QY	1024	GCACCCAGCGCCCTCTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	1083
Db	921	GCACCCAGCGCCCTCTGGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC	980
QY	1084	CAAAGGAGCAGCAGCACAATCTCAAGTCTCTGAGGAGAAACATAGAAAGCT	1143
Db	981	CAAAGGAGCAGCAGCACAATCTCAAGTCTCTGAGGAGAAACATAGAAAGCT	1040
QY	1144	GTGTGATGCGGGAAGACGTATCTCCAGGAGGTGTGGCACCGGCTTCCTGGCT	1203
Db	1041	GTGTGATGCGGGAAGACGTATCTCCAGGAGGTGTGGCACCGGCTTCCTGGCT	1100
QY	1204	TCGCGCCCTTGCTGCTCTCTATGCACTCTGTAGGATGGCCGCCAGGACTTCGACGGT	1263
Db	1101	TCGCGCCCTTGCTGCTCTCTATGCACTCTGTAGGATGGCCGCCAGGACTTCGACGGT	1160
QY	1264	TGACTCTGCTCCAGGATACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1323
Db	1161	TGACTCTGCTCCAGGATACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1220
QY	1324	AGATTTGCCAGAGACAAAGCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1383
Db	1221	AGATTTGCCAGAGACAAAGCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1280
QY	1384	CAAAGGACCGGCGCGGCTCTCTCTCAGATCTCTCAGATCTCTCAGATCTCTCAGATCTCTC	1443
Db	1281	CAAAGGACCGGCGCGGCTCTCTCTCAGATCTCTCAGATCTCTCAGATCTCTCAGATCTCTC	1340

RESULT 40

US-10-176-759-281
; Sequence 281, Application US/10176759
; Publication No. US20030166128A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P34301C80
; CURRENT APPLICATION NUMBER: US/10/176,759
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 281
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-759-281

Query Match 73.9%; Score 1342.8; DB 13; Length 1732; Best Local Similarity 97.7%; Pred. No. 0; Matches 1362; Conservative 0; Mismatches 32; Indels 0; Gaps 0;									
Qy	424	TTGGGCTGGAGCCTCTCGGACTAAATCATGGCACTGGTCGGTTTCCAGGCGCCAGACATGT	483						
Db	321	TGGGACTTCGGCTGTCTGTGTTCCCTCCAGCTCCACGCTCGAGCCCGCCAGACATGT	380						
Qy	484	TCTGCTTTTCATGGGAGAGATATCTCCCGGCGAGAGCTGCACCCCTACTTGGAGC	543						
Db	381	TCTGCTTTTCATGGGAGAGATATCTCCCGGCGAGAGCTGCACCCCTACTTGGAGC	440						
Qy	544	CACAGGCGCTGATGTACTGCTGCTGCTGTACTGCTGTACTGCTGTACTGCTGTACTGCTGT	603						

Db 441 CACAAGGCTGATGTACTCGCTGCGCTGTACTCTGCTCAGAGGGGCGCCCATGTGAGTTGTT 500
QY 604 ACCGCTCCACTGTCGCGCTGTCTCACTGCCCCCAGAGCTGTGACGGAGCCACAGCAATGCT 663
Db 501 ACCGCTCCACTGTCGCGCTGTCTCACTGCCCCCAGAGCTGTGACGGAGCCACAGCAATGCT 560
QY 664 GTCCCAAGTGTGTGGAAGCTCAGCTCCCTCTGAGATCCGGGCCCCACCAAGTCTCGCC 723
Db 561 GTCCCAAGTGTGTGGAAGCTCAGCTCCCTCTGAGATCCGGGCCCCACCAAGTCTCGCC 620
QY 724 AGCAACAAGGAGCAATGTATCCAAACGAGAGAGATCTTCACTGTCGCCATGAGTGTTCCTCT 783
Db 621 AGCAACAAGGAGCAATGTATCCAAACGAGAGAGATCTTCACTGTCGCCATGAGTGTTCCTCT 680
QY 784 CCGGCTGCTCCCAACCAAGTGTGTCTCTCACTGTCGCCAGAGGGCCAGATCTTCTGCGGCC 843
Db 681 CCGGCTGCTCCCAACCAAGTGTGTCTCTCACTGTCGCCAGAGGGCCAGATCTTCTGCGGCC 740
QY 844 TCACAACCTGCCCCCGAAGCAGGCTGCCAGCACCCCTCCGCTGCCAGATCTCTGTGTGCC 903
Db 741 TCACAACCTGCCCCCGAAGCAGGCTGCCAGCACCCCTCCGCTGCCAGATCTCTGTGTGCC 800
QY 904 AGCCTGCAAGATGAGGCAATGTGAGCAATCGGATGAAGGAGGACAGATGTGCACTCGCTCC 963
Db 801 AGCCTGCAAGATGAGGCAATGTGAGCAATCGGATGAAGGAGGACAGATGTGCACTCGCTCC 860
QY 964 ATGGGCTGAGACATCTCTAGATTCATATGTCAGTATGTCGGAGAAAGAGAGGCCGCG 1023
Db 861 ATGGGCTGAGACATCTCTAGATTCATATGTCAGTATGTCGGAGAAAGAGAGGCCGCG 920
QY 1024 GCACCCAGGCCCCCACTGGGCTCAGGGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 1083
Db 921 GCACCCAGGCCCCCACTGGGCTCAGGGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGAC 980
QY 1084 CCAAGGAGAGGAGGAGCAGACAACTGTCAAGATCTGCTGAAGGAGAAACATAAGAAAGCCT 1143
Db 981 CCAAGGAGAGGAGGAGCAGACAACTGTCAAGATCTGCTGAAGGAGAAACATAAGAAAGCCT 1040
QY 1144 GTGTGATGCGGGAGAGCACTACTCCACGGGGAGGTGTGGCACCGGCTTCGGTCCCT 1203
Db 1041 GTGTGATGCGGGAGAGCACTACTCCACGGGGAGGTGTGGCACCGGCTTCGGTCCCT 1100
QY 1204 TCGGCCCTTCCCTGATCCTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGCGTG 1263
Db 1101 TCGGCCCTTCCCTGATCCTATGCACTGTGAGGATGGCCCGCAGGACTGCCAGCGTG 1160
QY 1264 TGACCTGTCCACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGAAAGTGTGTGCA 1323
Db 1161 TGACCTGTCCACCGAGTACCCCTGCGCTCACCCCGAGAAAGTGGCTGGAAAGTGTGTGCA 1220
QY 1324 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAATCACTTACCAAGTGTGTC 1383
Db 1221 AGATTTGCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAATCACTTACCAAGTGTGTC 1280
QY 1384 CCAAGGCAACCGGGCGGGTCTCTGTCCACATCGGTATCCCAAGCCCGACACAACTGC 1443
Db 1281 CCAAGGCAACCGGGCGGGTCTCTGTCCACATCGGTATCCCAAGCCCGACACAACTGC 1340
QY 1444 GTGGCTTTTCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAAGTGG 1503
Db 1341 GTGGCTTTTCCCTGGAACACAGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAAGTGG 1400
QY 1504 TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCC 1563
Db 1401 TAAAGATGAGAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCC 1460
QY 1564 AGAATCTTCACTTCACTCAGATCAGAAAGTCCAGAGCAGAGCTCCAGAAAGGCA 1623
Db 1461 AGAATCTTCACTTCACTCAGATCAGAAAGTCCAGAGCAGAGCTCCAGAAAGGCA 1520
QY 1624 CAGCACTTCCGACTGCTCGTGGCCCCCAAGAGTCACTGGAAAGTCTTCTAGCCGAG 1683
Db 1521 CAGCACTTCCGACTGCTCGTGGCCCCCAAGAGTCACTGGAAAGTCTTCTAGCCGAG 1580

QY 1684 ACCCTGGAGCTGAAGGTCAAGCCAGTCCAGACAAAGTGAACAGACATTAACAAGACCT 1743
Db 1581 ACCCTGGAGCTGAAGGTCAAGCCAGTCCAGACAAAGTGAACAGACATTAACAAGACCT 1640
QY 1744 AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATTAATAAAGAAAGTTG 1803
Db 1641 AACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATTAATAAAGAAAGTTG 1700
QY 1804 CATACCATCAAAA 1817
Db 1701 CATACCATCAAAA 1714

Search completed: January 31, 2004, 06:00:50
Job time : 656 secs